

NR Native PVIIA Search:

**BLASTP 2.2.4 [Aug-26-2002]**

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038287392-07658-24371

**Query=**

(27 letters)

**Database:** All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,242,768 sequences; 395,571,179 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

**Distribution of 156 Blast Hits on the Query Sequence**

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Sequences producing significant alignments:	Score (bits)	E Value
gi 7519866 pir  A58997 kappa-conotoxin PVIIA - cone shell (...)	98	9e-21
gi 22002036 sp P56633 CXK7 CONPU Kappa-conotoxin PVIIA prec...	98	9e-21
gi 3891872 pdb 1KCP  3d Structure Of K-Conotoxin Pviia, A ...	93	4e-19
gi 3891964 pdb 1AV3  Potassium Channel Blocker Kappa Conot...	93	4e-19
gi 1905981 gb AAB50229.1  Gal/GalNAc lectin heavy subunit [...]	33	0.32
gi 17158399 ref NP_477819.1  wsv297 [shrimp white spot synd...	30	2.5
gi 15895618 ref NP_348967.1  Glycosyltransferase [Clostridi...	29	8.1
gi 10120503 pdb 1C6W A Chain A, Maurocalcin From Scorpio Ma...	28	11
gi 19577387 emb CAD27769.1  hypothetical protein [Anopheles...	28	11
gi 21402496 ref NP_658481.1  minC, Bacterial proteins invol...	28	15
gi 23021387 gb ZP_00061064.1  hypothetical protein [Clostri...	28	15
gi 17567271 ref NP_510129.1  Predicted CDS, p-glycoprotein ...	28	15
gi 20454175 gb AAM22197.1 AF501276_1 Gal/GalNAc lectin heav...	27	19
gi 7494127 pir  T09229 galactose binding adhesin heavy chai...	27	19

gi 22476954 gb AAM97358.1	Gal/GalNAc lectin heavy subunit ...	27	19
gi 2133404 pir S70663	lectin heavy chain, N-acetylgalactos...	27	19
gi 22964283 gb ZP_00011889.1	hypothetical protein [Rhodops...	27	19
gi 17563788 ref NP_507195.1	Predicted CDS, 7 transmembrane...	27	26
gi 21703938 ref NP_663450.1	ceramide kinase [Mus musculus]...	27	26
gi 543793 sp P36953 AFAM RAT	Afamin precursor (Alpha-albumi...	27	26
gi 23510111 ref NP_702777.1	erythrocyte membrane protein 1...	27	35
gi 17508479 ref NP_493155.1	Nuclear Hormone Receptor famil...	27	35
gi 17569649 ref NP_510122.1	Predicted CDS, zinc finger C4 ...	26	47
gi 23612818 ref NP_704357.1	hypothetical protein [Plasmodi...	26	47
gi 23613070 ref NP_703392.1	hypothetical protein [Plasmodi...	26	63
gi 23123030 gb ZP_00105165.1	hypothetical protein [Prochlo...	26	63
gi 21302332 gb EAA14477.1	agCP8528 [Anopheles gambiae str....	26	63
gi 21288202 gb EAA00523.1	agCP9342 [Anopheles gambiae str....	26	63
gi 17538866 ref NP_501730.1	Zinc finger C4 type Ligand-bin...	25	85
gi 17068427 gb AAH17594.1 AAH17594	Unknown (protein for MGC...	25	85
gi 17567269 ref NP_510128.1	P-glycoprotein family member (...)	25	85
gi 20454177 gb AAM22198.1 AF501277.1	Gal/GalNAc lectin heav...	25	85
gi 2133405 pir S70664	lectin heavy chain, N-acetylgalactos...	25	85
gi 11359716 pir  T46722	conserved hypothetical protein [imp...	25	85
gi 23510154 ref NP_702820.1	RNA-binding protein of pumilio...	25	85
gi 15450391 gb AAK96489.1	At2g16530/F1P15.9 [Arabidopsis t...	25	85
gi 20454179 gb AAM22199.1 AF501278.1	Gal/GalNAc lectin heav...	25	85
gi 6322428 ref NP_012502.1	Protein required for cell viabi...	25	85
gi 14250071 gb AAH08440.1 AAH08440	Similar to CGI-29 protei...	25	85
gi 8953421 emb CAB96572.1	AmphiGli protein [Branchiostoma ...	25	85
gi 399540 sp P32022 GIL1 ENTHI	GALACTOSE-INHIBITABLE LECTIN...	25	85
gi 14290597 gb AAH09077.1 AAH09077	CGI-29 protein [Homo sap...	25	85
gi 7705724 ref NP_057041.1	CGI-29 protein [Homo sapiens] >...	25	85
gi 10638481 emb CAC12642.1	dJ179L10.2 (Similar to CGI-29 p...	25	85
gi 7496642 pir  T19540	hypothetical protein C28D4.1 - Caeno...	25	85
gi 17569651 ref NP_510121.1	Nuclear receptor-like, contain...	25	114
gi 7513590 pir  T42230	AF4 protein - mouse (fragment) >gi 2...	25	114
gi 7661970 ref NP_055455.1	KIAA0173 gene product [Homo sap...	25	114
gi 159019 gb AAA29126.1	alpha-phosphoinositide-specific p...	25	114
gi 17563970 ref NP_506967.1	Zinc finger C4 type family mem...	25	114
gi 125493 sp P07313 KML2 RABIT	Myosin light chain kinase 2,...	25	114
gi 13359167 dbj BAB33316.1	KIAA1646 protein [Homo sapiens]	25	114
gi 17566198 ref NP_507649.1	Predicted CDS, zinc finger C4 ...	25	114
gi 6572330 emb CAB62977.1	da59H18.2 (novel protein similar...	25	114
gi 20898146 ref XP_127515.1	similar to hypothetical protei...	25	114
gi 7662550 ref NP_054801.1	PRQ0397 protein [Homo sapiens] ...	25	114
gi 25023945 ref XP_204197.1	homolog of human MLLT2 unident...	25	114
gi 125494 sp P20689 KML2 RAT	Myosin light chain kinase 2, s...	25	114
gi 20849986 ref XP_138040.1	similar to ribosomal protein S...	25	114
gi 21553101 ref NP_660128.1	afamin precursor; alpha albumi...	25	114
gi 14993776 ref NP_149109.1	skeletal myosin light chain ki...	25	114
gi 17105364 ref NP_476557.1	myosin light chain kinase 2, s...	25	114
gi 20072386 gb AAH26681.1	Unknown (protein for IMAGE:50644...	25	114
gi 20336726 ref NP_073603.2	ceramide kinase; lipid kinase ...	25	114
gi 13878317 sp O88573 AF4 MOUSE	AF-4 protein (Proto-oncogen...	25	114
gi 393063 gb AAA18296.1	hemagglutinin-neuraminidase >gi 39...	24	153
gi 1621417 gb AAB17181.1	hemagglutinin-neuraminidase [Huma...	24	153
gi 393067 gb AAA03318.1	hemagglutinin-neuraminidase	24	153
gi 1621397 gb AAB17171.1	hemagglutinin-neuraminidase [Huma...	24	153
gi 393053 gb AAA18291.1	hemagglutinin-neuraminidase	24	153
gi 17544200 ref NP_502862.1	Putative secreted or extracell...	24	153
gi 25155182 ref NP_741645.1	Nuclear Hormone Receptor famil...	24	153
gi 1621421 gb AAB17183.1	hemagglutinin-neuraminidase [Huma...	24	153
gi 393047 gb AAA18288.1	hemagglutinin-neuraminidase	24	153
gi 13878219 ref NP_113566.1	ribonuclease/angiogenin inhibi...	24	153

<u>gi 393059 gb AAA18294.1 </u>	hemagglutinin-neuraminidase	24	153
<u>gi 1621409 gb AAB17177.1 </u>	hemagglutinin-neuraminidase [Huma...	24	153
<u>gi 1621413 gb AAB17179.1 </u>	hemagglutinin-neuraminidase [Huma...	24	153
<u>gi 1621405 gb AAB17175.1 </u>	hemagglutinin-neuraminidase [Huma...	24	153
<u>gi 1621419 gb AAB17182.1 </u>	hemagglutinin-neuraminidase [Huma...	24	153
<u>gi 729836 sp P41323 IL6_CANFA</u>	Interleukin-6 precursor (IL-6...	24	153
<u>gi 9629903 ref NP 045936.1 </u>	ORF-C [Walleye dermal sarcoma v...	24	153
<u>gi 393051 gb AAA18290.1 </u>	hemagglutinin-neuraminidase	24	153
<u>gi 13027596 ref NP 076421.1 </u>	hypothetical protein MGC2487 [...	24	153
<u>gi 15231494 ref NP 189706.1 </u>	hypothetical protein; protein ...	24	153
<u>gi 19263653 gb AAH25255.1 </u>	Similar to hypothetical protein ...	24	153
<u>gi 22507470 gb AAH19431.1 </u>	Similar to hypothetical protein ...	24	153
<u>gi 12383068 ref NP 073738.1 </u>	hypothetical protein FLJ21347 ...	24	153
<u>gi 9247084 gb AAF86275.1 </u>	interleukin-6 [Canis familiaris]	24	153
<u>gi 19921116 ref NP 609448.1 </u>	CG12299-PA [Drosophila melanog...	24	153
<u>gi 393049 gb AAA18289.1 </u>	hemagglutinin-neuraminidase	24	153
<u>gi 1621415 gb AAB17180.1 </u>	hemagglutinin-neuraminidase [Huma...	24	153
<u>gi 1621399 gb AAB17172.1 </u>	hemagglutinin-neuraminidase [Huma...	24	153
<u>gi 393069 gb AAA03319.1 </u>	hemagglutinin-neuraminidase	24	153
<u>gi 1621411 gb AAB17178.1 </u>	hemagglutinin-neuraminidase [Huma...	24	153
<u>gi 16588867 gb AAL26923.1 AF328929 1</u>	interleukin-6 [Canis f...	24	153
<u>gi 10198059 gb AAG15164.1 </u>	nuclear receptor NHR-63 [Caenorh...	24	153
<u>gi 23507986 ref NP 700656.1 </u>	hypothetical protein [Plasmodi...	24	153
<u>gi 1621403 gb AAB17174.1 </u>	hemagglutinin-neuraminidase [Huma...	24	153
<u>gi 1621407 gb AAB17176.1 </u>	hemagglutinin-neuraminidase [Huma...	24	153

### Alignments

Get selected sequences  
 Select all  
 Deselect all

>gi|7519866|pir||A58997 kappa-conotoxin PVIIA - cone shell (Conus purpurascens)  
 Length = 27

Score = 98.2 bits (224), Expect = 9e-21  
 Identities = 27/27 (100%), Positives = 27/27 (100%)

Query: 1 CRIPNQKCFQHLDCCSRKCNRFNKC 27  
 CRIPNQKCFQHLDCCSRKCNRFNKC  
 Sbjct: 1 CRIPNQKCFQHLDCCSRKCNRFNKC 27

>gi|22002036|sp|P56633|CXK7 CONPU Kappa-conotoxin PVIIA precursor (Fin-popping peptide)  
 Length = 72

Score = 98.2 bits (224), Expect = 9e-21  
 Identities = 27/27 (100%), Positives = 27/27 (100%)

Query: 1 CRIPNQKCFQHLDCCSRKCNRFNKC 27  
 CRIPNQKCFQHLDCCSRKCNRFNKC  
 Sbjct: 46 CRIPNQKCFQHLDCCSRKCNRFNKC 72

>gi|3891872|pdb|1KCP| 3d Structure Of K-Conotoxin Pviiia, A Novel Potassium  
 Channel-Blocking Toxin From Cone Snails, Nmr, 22

Structures  
Length = 28

Score = 92.7 bits (211), Expect = 4e-19  
Identities = 26/27 (96%), Positives = 26/27 (96%)

Query: 1 CRIPNQKCFQHLDCCSRKCNRFNKC 27  
CRI NQKCFQHLDCCSRKCNRFNKC  
Sbjct: 1 CRIXNQKCFQHLDCCSRKCNRFNKC 27

>gi|3891964|pdb|1AV3| Potassium Channel Blocker Kappa Conotoxin Pviia From C.  
Purpurascens, Nmr, 20 Structures  
Length = 27

Score = 92.7 bits (211), Expect = 4e-19  
Identities = 26/27 (96%), Positives = 26/27 (96%)

Query: 1 CRIPNQKCFQHLDCCSRKCNRFNKC 27  
CRI NQKCFQHLDCCSRKCNRFNKC  
Sbjct: 1 CRIXNQKCFQHLDCCSRKCNRFNKC 27

>gi|1905981|gb|AAB50229.1| Gal/GalNAc lectin heavy subunit [Entamoeba dispar]  
Length = 1125

Score = 33.3 bits (71), Expect = 0.32  
Identities = 12/17 (70%), Positives = 12/17 (70%), Gaps = 3/17 (17%)

Query: 13 DDCCSRK--CNRFN-KC 26  
DDCCSRK C FN KC  
Sbjct: 700 DDCCSRKSQCGNFNGKC 716

>gi|17158399|ref|NP\_477819.1| wsv297 [shrimp white spot syndrome virus]  
gi|17016693|gb|AAL33299.1| wsv297 [shrimp white spot syndrome virus]  
gi|19481945|gb|AAL89221.1| WSSV353 [shrimp white spot syndrome virus]  
Length = 69

Score = 30.3 bits (64), Expect = 2.5  
Identities = 9/14 (64%), Positives = 10/14 (71%), Gaps = 3/14 (21%)

Query: 12 LDDCCSRKCNRFNK 25  
LD+CC CNRF K  
Sbjct: 29 LDECC---CNRFQK 39

>gi|15895618|ref|NP\_348967.1| Glycosyltransferase [Clostridium acetobutylicum]  
gi|15025361|gb|AAK80307.1|AE007735 10 Glycosyltransferase [Clostridium acetobutylicum]  
Length = 252

Score = 28.6 bits (60), Expect = 8.1  
Identities = 11/24 (45%), Positives = 13/24 (54%), Gaps = 11/24 (45%)

Query: 8 CFQHLDCCSRK-----CNRFN 24  
CF ++DCC K CNRFN  
Sbjct: 193 CF--IEDCC--KQGIKIYSCNRFN 212

>gi|10120503|pdb|1C6W|A Chain A, Maurocalcin From Scorpio Maurus  
 Length = 33

Score = 28.2 bits (59), Expect = 11  
 Identities = 10/21 (47%), Positives = 11/21 (52%), Gaps = 6/21 (28%)

Query: 8 CFQHLD-----DCCSRKCNR 22  
 C HL DCCS+KC R  
 Sbjct: 3 CLPHLKLCKENKDCCSKKCKR 23

>gi|19577387|emb|CAD27769.1| hypothetical protein [Anopheles gambiae]  
 Length = 257

Score = 28.2 bits (59), Expect = 11  
 Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 15 CCSRKCNR 22  
 CCSRKC+R  
 Sbjct: 41 CCSRKCSR 48

>gi|21402496|ref|NP\_658481.1| minC, Bacterial proteins involved in chromosomal partitioning  
 [Bacillus anthracis A2012]  
 Length = 228

Score = 27.8 bits (58), Expect = 15  
 Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 11 HLDDCCS 17  
 HLDDCCS  
 Sbjct: 21 HLDDCCS 27

>gi|23021387|gb|ZP\_00061064.1| hypothetical protein [Clostridium thermocellum ATCC 27405]  
 Length = 143

Score = 27.8 bits (58), Expect = 15  
 Identities = 9/18 (50%), Positives = 11/18 (61%), Gaps = 4/18 (22%)

Query: 14 DC----CSRKCNRFNKCV 27  
 DC S KC+RF+ CV  
 Sbjct: 91 DCVVEDSSPKCDRFDNCV 108

>gi|17567271|ref|NP\_510129.1| Predicted CDS, p-glycoprotein family member  
 [Caenorhabditis elegans]  
 gi|7499666|pir||T21269 hypothetical protein F22E10.4 - Caenorhabditis elegans  
 gi|3876294|emb|CAA91802.1| C. elegans pgp-15 protein (corresponding sequence F22E10.4)  
 [Caenorhabditis elegans]  
 Length = 1270

Score = 27.8 bits (58), Expect = 15  
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 8 CFQHLDDCSR 18  
 CFQH CCSR  
 Sbjct: 165 CFQH---CCSR 172

>gi|20454175|gb|AAM22197.1|AF501276 1 Gal/GalNAc lectin heavy subunit region D  
 [Entamoeba histolytica]  
 Length = 372

Score = 27.4 bits (57), Expect = 19  
 Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KCV  
 Sbjct: 92 DDCNSRKSQCGNFNGKCV 109

>gi|7494127|pir||T09229 galactose binding adhesin heavy chain - Entamoeba histolytica  
 gi|290649|gb|AAA18828.1| galactose-specific adhesin 170kD subunit  
 Length = 1292

Score = 27.4 bits (57), Expect = 19  
 Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KCV  
 Sbjct: 730 DDCNSRKSQCGNFNGKCV 747

>gi|22476954|gb|AAM97358.1| Gal/GalNAc lectin heavy subunit region D [Entamoeba histolytica]  
 Length = 372

Score = 27.4 bits (57), Expect = 19  
 Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KCV  
 Sbjct: 92 DDCNSRKSQCGNFNGKCV 109

>gi|2133404|pir||S70663 lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment)  
 gi|993053|gb|AAA75551.1| GalNAc lectin heavy subunit  
 Length = 194

Score = 27.4 bits (57), Expect = 19  
 Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KCV  
 Sbjct: 131 DDCNSRKSQCGNFNGKCV 148

>gi|22964283|gb|ZP\_00011889.1| hypothetical protein [Rhodopseudomonas palustris]  
 Length = 559

Score = 27.4 bits (57), Expect = 19  
 Identities = 9/12 (75%), Positives = 10/12 (83%), Gaps = 1/12 (8%)

Query: 8 CFQHLDDCCSRK 19  
 C+QHLDD SRK  
 Sbjct: 49 CYQHLDD-ISRK 59

>gi|17563788|ref|NP\_507195.1| Predicted CDS, 7 transmembrane chemoreceptor family member family

member [Caenorhabditis elegans]

gi|7506996|pir||T24389 hypothetical protein T03E6.2 - Caenorhabditis elegans

gi|3879369|emb|CAB07277.1| Hypothetical protein T03E6.2 [Caenorhabditis elegans]  
 Length = 213

Score = 26.9 bits (56), Expect = 26  
 Identities = 8/13 (61%), Positives = 9/13 (69%), Gaps = 3/13 (23%)

Query: 1 CR---IPNQKCFQ 10  
 CR + NQKCFQ  
 Sbjct: 55 CRTMLVSNQKCFQ 67

Score = 20.2 bits (40), Expect = 2886  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 5 NQKCFQ 10  
 N+KCFQ  
 Sbjct: 125 NRKCFQ 130

>gi|21703938|ref|NP\_663450.1| ceramide kinase [Mus musculus]

gi|21624342|dbj|BAC01155.1| ceramide kinases [Mus musculus]

Length = 531

Score = 26.9 bits (56), Expect = 26  
 Identities = 11/21 (52%), Positives = 12/21 (57%), Gaps = 5/21 (23%)

Query: 9 FQHLDDCCS----RKCNRFN 24  
 F HL D S RKC+RFN  
 Sbjct: 410 FAHLDGDGSSDLILIRKCSRNF 430

>gi|543793|sp|P36953|AFAM\_RAT Afamin precursor (Alpha-albumin) (Alpha-Alb)

gi|1363266|pir||A53195 afamin precursor - rat

gi|456359|emb|CAA53994.1| unnamed protein product [Rattus norvegicus]

Length = 608

Score = 26.9 bits (56), Expect = 26  
 Identities = 10/22 (45%), Positives = 12/22 (54%), Gaps = 9/22 (40%)

Query: 12 LDDCCSRK----CNR----FN 24  
 L+DCC+RK C R FN  
 Sbjct: 381 LEDCCNRKNPLSCYRHAEDKFN 402

Score = 18.5 bits (36), Expect = 9354  
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 8 CFQHL 12  
 CF+HL  
 Sbjct: 509 CFEHL 513

>gi|23510111|ref|NP\_702777.1| erythrocyte membrane protein 1 (PfEMP1) [Plasmodium falciparum 3D7]  
 gi|6562758|emb|CAB62897.1| erythrocyte membrane protein 1 (PfEMP1) [Plasmodium falciparum 3D7]  
 Length = 2209

Score = 26.5 bits (55), Expect = 35  
 Identities = 12/24 (50%), Positives = 15/24 (62%), Gaps = 8/24 (33%)

Query: 9 FQHLDDC--CSR---KC-NRFNKC 26  
 FQH +DC CS+ KC N +KC  
 Sbjct: 1356 FQHTEDCKSCSKFRIKCDN--DKC 1377

>gi|17508479|ref|NP\_493155.1| Nuclear Hormone Receptor family NHR-89 (nhr-89) [Caenorhabditis elegans]  
 gi|7498355|pir||T20208 hypothetical protein E03H4.13 - Caenorhabditis elegans  
 gi|3875219|emb|CAB05470.1| C. elegans nhr-89 protein (corresponding sequence E03H4.13) [Caenorhabditis elegans]  
 gi|3875498|emb|CAB04035.1| C. elegans nhr-89 protein (corresponding sequence E03H4.13) [Caenorhabditis elegans]  
 Length = 310

Score = 26.5 bits (55), Expect = 35  
 Identities = 11/20 (55%), Positives = 12/20 (60%), Gaps = 7/20 (35%)

Query: 12 LDD----CCSRKCNRFNKC 27  
 LDD C R C R+NKCV  
 Sbjct: 52 LDDQKQFC--RSC-RYNKCV 68

>gi|17569649|ref|NP\_510122.1| Predicted CDS, zinc finger C4 type Ligand-binding domain of  
 nuclear hormone receptor like family member [Caenorhabditis elegans]  
 gi|7507363|pir||T24650 hypothetical protein T07C5.2 - Caenorhabditis elegans  
 gi|3879537|emb|CAA90299.1| Hypothetical protein T07C5.2 [Caenorhabditis elegans]  
 Length = 334

Score = 26.1 bits (54), Expect = 47  
 Identities = 12/26 (46%), Positives = 13/26 (50%), Gaps = 12/26 (46%)

Query: 2 RIPNQKCFQHLDCCSRKCNRFNKC 27

R+P KC R C RFNKC  
 Sbjct: 59 RLP--KC-----RHC-RFNKC 72

>gi|23612818|ref|NP\_704357.1| hypothetical protein [Plasmodium falciparum 3D7]  
 gi|23499096|emb|CAD51176.1| hypothetical protein [Plasmodium falciparum 3D7]  
 Length = 1408

Score = 26.1 bits (54), Expect = 47  
 Identities = 11/20 (55%), Positives = 12/20 (60%), Gaps = 8/20 (40%)

Query: 6 QKCFQHLDDCCSRKCNRFNK 25  
 +KCF D SRKCN NK  
 Sbjct: 1008 EKCF---D---SRKCN--NK 1019

>gi|23613070|ref|NP\_703392.1| hypothetical protein [Plasmodium falciparum 3D7]  
 gi|23504532|emb|CAD51412.1| hypothetical protein [Plasmodium falciparum 3D7]  
 Length = 2349

Score = 25.7 bits (53), Expect = 63  
 Identities = 9/14 (64%), Positives = 11/14 (78%), Gaps = 1/14 (7%)

Query: 12 LDDCCSRKCN-RFN 24  
 LDD C+ KCN +FN  
 Sbjct: 1975 LDDICNNKCNDFN 1988

Score = 17.6 bits (34), Expect = 16841  
 Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 19 KCNRFN 24  
 K NRFN  
 Sbjct: 359 KINRFN 364

>gi|23123030|gb|ZP\_00105165.1| hypothetical protein [Prochlorococcus marinus subsp. *pastoris* str.  
 CCMP1378]  
 Length = 284

Score = 25.7 bits (53), Expect = 63  
 Identities = 7/10 (70%), Positives = 9/10 (90%)

Query: 10 QHLDCCSRK 19  
 +HL +CCSRK  
 Sbjct: 211 EHLINCCSRK 220

>gi|21302332|gb|EAA14477.1| agCP8528 [Anopheles gambiae str. PEST]  
 Length = 851

Score = 25.7 bits (53), Expect = 63  
 Identities = 8/15 (53%), Positives = 10/15 (66%), Gaps = 3/15 (20%)

Query: 16 CSRKCN---RFNKC 27

C RKC+ RF +CV  
 Sbjct: 49 CRRKCDRACRGRCV 63

>gi|21288202|gb|EAA00523.1| agCP9342 [Anopheles gambiae str. PEST]  
 Length = 382

Score = 25.7 bits (53), Expect = 63  
 Identities = 12/32 (37%), Positives = 17/32 (53%), Gaps = 12/32 (37%)

Query: 1 CRIPN--QKC----FQHLDDCCSRKCNRFNKC 26  
 C +P+ +KC F H DDC ++F KC  
 Sbjct: 160 CPVPDTCEKCDPTFFPH-DDC-----DKFYKC 185

>gi|17538866|ref|NP\_501730.1| Zinc finger C4 type Ligand-binding domain of nuclear  
 hormone

receptor like family member [Caenorhabditis elegans]

gi|15718178|emb|CAC70072.1| Hypothetical protein C28D4.9 [Caenorhabditis elegans]  
 Length = 420

Score = 25.2 bits (52), Expect = 85  
 Identities = 11/24 (45%), Positives = 12/24 (50%), Gaps = 11/24 (45%)

Query: 13 DDC-----CSRKCNRFNKCV 27  
 +DC C R C RFNKC  
 Sbjct: 54 EDCEVLQQFRNRC-RAC-RFNKC 75

>gi|17068427|gb|AAH17594.1|AAH17594| Unknown (protein for MGC:714) [Homo sapiens]  
 Length = 242

Score = 25.2 bits (52), Expect = 85  
 Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
 DCCSR+C  
 Sbjct: 10 DCCSRRC 16

>gi|17567269|ref|NP\_510128.1| P-glycoprotein family member (146.9 kD) [Caenorhabditis  
 elegans]  
gi|7499665|pir|T21268| hypothetical protein F22E10.3 - Caenorhabditis elegans  
gi|3876293|emb|CAA91801.1| C. elegans pgp-14 protein (corresponding sequence F22E10.3)  
 [Caenorhabditis elegans]  
 Length = 1327

Score = 25.2 bits (52), Expect = 85  
 Identities = 7/11 (63%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 8 CFQHLDDCCSR 18  
 CFQH CC+R  
 Sbjct: 171 CFQH---CCTR 178

>gi|20454177|gb|AAM22198.1|AF501277 1 Gal/GalNAc lectin heavy subunit region D  
 [Entamoeba histolytica]  
 Length = 372

Score = 25.2 bits (52), Expect = 85  
 Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KC+  
 Sbjct: 92 DDCNSRKSQCGNFNGKCI 109

>gi|2133405|pir||S70664 lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment)  
 gi|993055|gb|AAA75552.1| GalNAc lectin heavy subunit  
 Length = 194

Score = 25.2 bits (52), Expect = 85  
 Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KC+  
 Sbjct: 131 DDCNSRKSQCGNFNGKCI 148

>gi|11359716|pir||T46722 conserved hypothetical protein [imported] - Leishmania major  
 gi|6066445|emb|CAB58387.1| possible proline synthetase associated protein [Leishmania major]  
 Length = 389

Score = 25.2 bits (52), Expect = 85  
 Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
 DCCSR+C  
 Sbjct: 89 DCCSRRC 95

>gi|23510154|ref|NP\_702820.1| RNA-binding protein of pumilio/mpt5 family, putative [Plasmodium falciparum 3D7]  
 gi|23498236|emb|CAD49207.1| RNA-binding protein of pumilio/mpt5 family, putative [Plasmodium falciparum 3D7]  
 gi|24849851|gb|AAM44411.1| RNA-binding protein Puf2 [Plasmodium falciparum]  
 Length = 514

Score = 25.2 bits (52), Expect = 85  
 Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 6 QKCFQHLDD 14  
 QKCF+H DD  
 Sbjct: 392 QKCFEHSD 400

>gi|15450391|gb|AAK96489.1| At2g16530/F1P15.9 [Arabidopsis thaliana]  
 Length = 343

Score = 25.2 bits (52), Expect = 85  
 Identities = 8/10 (80%), Positives = 8/10 (80%), Gaps = 1/10 (10%)

Query: 3 IPNQKCFQHL 12  
 IP QKCF HL  
 Sbjct: 61 IP-QKCFAHL 69

>gi|20454179|gb|AAM22199.1|AF501278 1 Gal/GalNAc lectin heavy subunit region D  
 [Entamoeba histolytica]  
 Length = 372

Score = 25.2 bits (52), Expect = 85  
 Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KC+  
 Sbjct: 92 DDCNSRKSQCGNFNGKCI 109

>gi|6322428|ref|NP\_012502.1| Protein required for cell viability; Yjl032wp  
 [Saccharomyces  
 cerevisiae]  
 gi|1352969|sp|P47059|YJD2 YEAST HYPOTHETICAL 12.4 KD PROTEIN IN DBP4-BET4 INTERGENIC  
 REGION  
 gi|1077805|pir||S56804 hypothetical protein YJL032w - yeast (Saccharomyces cerevisiae)  
 gi|1008152|emb|CAA89322.1| ORF YJL032w [Saccharomyces cerevisiae]  
 Length = 104

Score = 25.2 bits (52), Expect = 85  
 Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 2/12 (16%)

Query: 9 FQHLDCCSRKC 20  
 + HL CCSR+C  
 Sbjct: 6 YHHL--CCSRR 15

>gi|14250071|gb|AAH08440.1|AAH08440 Similar to CGI-29 protein [Homo sapiens]  
 Length = 242

Score = 25.2 bits (52), Expect = 85  
 Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
 DCCSR+C  
 Sbjct: 10 DCCSRRC 16

>gi|8953421|emb|CAB96572.1| AmphiGli protein [Branchiostoma floridae]  
 Length = 1112

Score = 25.2 bits (52), Expect = 85  
 Identities = 13/25 (52%), Positives = 13/25 (52%), Gaps = 8/25 (32%)

Query: 6 QKCFQHLDDC--CS--RKCNRFNKC 26  
 QKC C CS RKCNR KC

Sbjct: 1013 QKC----SKCKRCSKCRKCNRCKKC 1033

>gi|399540|sp|P32022|GILL ENTHI GALACTOSE-INHIBITABLE LECTIN 170 KD SUBUNIT  
Length = 1276

Score = 25.2 bits (52), Expect = 85  
Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
DDC SRK C FN KC+

Sbjct: 714 DDCNSRKSQCGNFNGKCI 731

>gi|14290597|gb|AAH09077.1|AAH09077 CGI-29 protein [Homo sapiens]  
Length = 242

Score = 25.2 bits (52), Expect = 85  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
DCCSR+C

Sbjct: 10 DCCSRRC 16

>gi|7705724|ref|NP\_057041.1| CGI-29 protein [Homo sapiens]  
gi|4680697|gb|AAD27738.1|AF132963 1 CGI-29 protein [Homo sapiens]  
Length = 242

Score = 25.2 bits (52), Expect = 85  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
DCCSR+C

Sbjct: 10 DCCSRRC 16

>gi|10638481|emb|CAC12642.1| dJ179L10.2 (Similar to CGI-29 protein) [Homo sapiens]  
Length = 153

Score = 25.2 bits (52), Expect = 85  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
DCCSR+C

Sbjct: 10 DCCSRRC 16

>gi|7496642|pir||T19540 hypothetical protein C28D4.1 - Caenorhabditis elegans  
Length = 874

Score = 25.2 bits (52), Expect = 85  
Identities = 11/24 (45%), Positives = 12/24 (50%), Gaps = 11/24 (45%)

Query: 13 DDC-----CSRKCNRFNKCV 27  
+DC C R C RFNKC

Sbjct: 96 EDCEVLQQFRNRC-RAC-RFNKCV 117

>gi|17569651|ref|NP\_510121.1| Nuclear receptor-like, contains ligand-binding domain but no

obvious zinc finger family member [Caenorhabditis elegans]

gi|7507364|pir||T24648 hypothetical protein T07C5.3 - Caenorhabditis elegans

gi|3879535|emb|CAA90297.1| Hypothetical protein T07C5.3 [Caenorhabditis elegans]

Length = 319

Score = 24.8 bits (51), Expect = 114

Identities = 8/10 (80%), Positives = 8/10 (80%), Gaps = 1/10 (10%)

Query: 18 RKCNRFNKCV 27

R C RFNKC

Sbjct: 49 RHC-RFNKCV 57

>gi|7513590|pir||T42230 AF4 protein - mouse (fragment)

gi|2582019|gb|AAB82427.1| mAF4 [Mus musculus]

Length = 1211

Score = 24.8 bits (51), Expect = 114

Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 16 CSRKCNR 22

CSRKC+R

Sbjct: 158 CSRKCDR 164

>gi|7661970|ref|NP\_055455.1| KIAA0173 gene product [Homo sapiens]

gi|20455377|sp|Q14679|Y173 HUMAN Hypothetical protein KIAA0173

gi|1136406|dbj|BAAl1490.1| similar to pig tubulin-tyrosine ligase. [Homo sapiens]

Length = 1199

Score = 24.8 bits (51), Expect = 114

Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 12 LDDCCSR 18

L+DCCSR

Sbjct: 519 LEDCCSR 525

>gi|159019|gb|AAA29126.1| alpha-phosphoinositide-specific phospholipase C-like protein

precursor [Euplotes crassus]

gi|228393|prf||1803429A phospholipase C-like protein

Length = 141

Score = 24.8 bits (51), Expect = 114

Identities = 10/16 (62%), Positives = 11/16 (68%), Gaps = 5/16 (31%)

Query: 12 LDDCCSR-K--CNRFN 24

LD CSR K C+RFN

Sbjct: 78 LD--CSRYKPVCDFN 91

```

>gi|17563970|ref|NP_506967.1|  Zinc finger C4 type family member (47.8 kD)
[Caenorhabditis
  elegans]
gi|7507276|pir||T24563  hypothetical protein T06C12.6 - Caenorhabditis elegans
gi|3879608|emb|CAB03298.1|  Hypothetical protein T06C12.6 [Caenorhabditis elegans]
Length = 414

Score = 24.8 bits (51), Expect = 114
Identities = 11/24 (45%), Positives = 12/24 (50%), Gaps = 11/24 (45%)

Query: 13 DDC-----CSRKCNRFNKCV 27
        D+C          C R C RFNKC
Sbjct: 67 DNCAVSSTDYQC-RLC-RFNKC 88

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Get selected sequences
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Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Nov 25, 2002 1:38 AM
Number of letters in database: 395,571,179
Number of sequences in database: 1,242,768

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Lambda      K      H
0.355      0.288    2.12

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Gapped
Lambda      K      H
0.294      0.110    0.610

```

```

Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Hits to DB: 21,155,857
Number of Sequences: 1242768
Number of extensions: 470271
Number of successful extensions: 11171
Number of sequences better than 20000.0: 10987
Number of HSP's better than 20000.0 without gapping: 10987
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 11165
length of query: 27
length of database: 395,571,179
effective HSP length: 18
effective length of query: 9
effective length of database: 373,201,355
effective search space: 3358812195
effective search space used: 3358812195
T: 11
A: 40
X1: 14 ( 7.2 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 34 (19.2 bits)

```

S2: 34 (17.6 bits)

Pat Native PVIIA Search

**BLASTP 2.2.4 [Aug-26-2002]**

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038287801-011156-13490

**Query=**

(27 letters)

**Database:** Protein sequences derived from the Patent division of GenBank

104,350 sequences; 16,453,681 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

[Distribution of 191 Blast Hits on the Query Sequence](#)

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Score (bits)	E Value
Sequences producing significant alignments:	
27	0.76
27	0.76
25	3.3
25	3.3
25	3.3
25	4.4
25	4.4
25	4.4
24	6.0
24	8.0
24	8.0
24	11
24	11
24	11
24	11

gi 4530800 emb CAA03825.1	unnamed protein product [unident...]	24	11
gi 3409412 gb AAC30467.1 I89472	Sequence 2 from patent US 5...	24	11
gi 3409416 gb AAC30471.1 I89476	Sequence 12 from patent US ...	24	11
gi 4530803 emb CAA03826.1	unnamed protein product [unident...]	24	11
gi 20221551 gb AAE87124.1	Sequence 11 from patent US 6326165	23	14
gi 12822272 gb AAE48713.1	Sequence 6 from patent US 6107088	23	14
gi 20221546 gb AAE87119.1	Sequence 4 from patent US 6326165	23	14
gi 12822270 gb AAE48711.1	Sequence 2 from patent US 6107088	23	14
gi 20221547 gb AAE87120.1	Sequence 5 from patent US 6326165	23	14
gi 16242616 gb AAE79920.1	Sequence 20 from patent US 6280975	23	19
gi 410755 emb CAA00367.1	P.195 [Plasmodium falciparum]	23	19
gi 15118603 gb AAE70697.1	Sequence 100 from patent US 6232061	22	26
gi 23330539 gb AAN26530.1	Sequence 2 from patent US 6432408	22	26
gi 15141755 emb CAC50180.1	Orf1 [Hepatitis E virus]	22	26
gi 1254372 gb AAA95626.1	Sequence 6 from patent US 5482928...	22	26
gi 20227333 gb AAE89374.1	Sequence 36 from patent US 63407...	22	26
gi 3209904 gb AAC20848.1 I81607	Sequence 2 from patent US 5...	22	26
gi 3991599 gb AAC85026.1 AR002030	Sequence 52 from patent U...	22	26
gi 15116726 gb AAE70252.1	Sequence 7 from patent US 622900...	22	26
gi 14484312 gb AAE63497.1	Sequence 1 from patent US 620741...	22	26
gi 1613525 gb AAB16505.1	Sequence 2 from patent US 5559095...	22	26
gi 1613542 gb AAB16522.1	Sequence 19 from patent US 555909...	22	35
gi 1613531 gb AAB16511.1	Sequence 8 from patent US 5559095...	22	35
gi 14092871 gb AAE51612.1	Sequence 4 from patent US 613003...	22	35
gi 4000083 gb AAC93515.1 AR023217	Sequence 55 from patent U...	21	47
gi 7224006 gb AAE24173.1	Sequence 2 from patent US 5891857...	21	47
gi 23342653 emb CAD48690.1	unnamed protein product [Homo s...	21	47
gi 5946864 gb AAE03769.1	Sequence 20 from patent US 586654...	21	47
gi 4000084 gb AAC93516.1 AR023218	Sequence 56 from patent U...	21	47
gi 3209905 gb AAC20849.1 I81608	Sequence 4 from patent US 5...	21	47
gi 14100343 gb AAE53483.1	Sequence 4 from patent US 6140485	21	47
gi 5946896 gb AAE03801.1	Sequence 62 from patent US 586654...	21	47
gi 15141758 emb CAC50182.1	Orf1 [Hepatitis E virus]	21	47
gi 23342657 emb CAD48692.1	unnamed protein product [Homo s...	21	47
gi 3014969 gb AAC11849.1 I78815	Sequence 2 from patent US 5...	21	47
gi 4000082 gb AAC93514.1 AR023216	Sequence 54 from patent U...	21	47
gi 1610962 gb AAB13941.1	Sequence 14 from patent US 5527896	21	47
gi 3210125 gb AAC21069.1 I81828	Sequence 6 from patent US 5...	21	47
gi 23342661 emb CAD48694.1	unnamed protein product [Homo s...	21	47
gi 10050761 gb AAE27668.1	Sequence 30 from patent US 5955318	21	47
gi 3936646 gb AAC80745.1 I92176	Sequence 8 from patent US 5...	21	47
gi 2489823 gb AAB77959.1 I60068	Sequence 2 from patent US 5...	21	47
gi 14035826 emb CAC38509.1	unnamed protein product [Homo s...	21	47
gi 592200 gb AAA53807.1	Sequence 4 from Patent WO 8909834	21	47
gi 3210124 gb AAC21068.1 I81827	Sequence 5 from patent US 5...	21	47
gi 10057493 gb AAE34399.1	Sequence 14 from patent US 5977305	21	47
gi 3994047 gb AAC87475.1 AR007841	Sequence 4 from patent US...	21	47
gi 4000081 gb AAC93513.1 AR023215	Sequence 53 from patent U...	21	47
gi 2095522 gb AAB54354.1	Sequence 23 from patent US 562282...	21	47
gi 912366 gb AAA71820.1	Sequence 25 from patent US 5429921...	21	47
gi 20268179 gb AAM17416.1	Sequence 49 from patent US 6361954	21	47
gi 5946869 gb AAE03774.1	Sequence 25 from patent US 586654...	21	47
gi 5946861 gb AAE03766.1	Sequence 7 from patent US 5866542...	21	47
gi 2095523 gb AAB54355.1	Sequence 24 from patent US 562282...	21	47
gi 2095515 gb AAB54347.1	Sequence 16 from patent US 562282...	21	47
gi 5946859 gb AAE03764.1	Sequence 4 from patent US 5866542...	21	47
gi 20246635 gb AAE95293.1	Sequence 111 from patent US 6350933	21	63
gi 2489301 gb AAB77437.1 I58938	Sequence 23 from patent US ...	21	63
gi 14118421 gb AAE59660.1	Sequence 90 from patent US 6187548	21	63
gi 2489300 gb AAB77436.1 I58937	Sequence 10 from patent US ...	21	63
gi 5946881 gb AAE03786.1	Sequence 47 from patent US 586654...	21	63

<u>gi 17912954 gb AAE83208.1 </u>	Sequence 33 from patent US 6303295	<u>21</u>	63
<u>gi 21260774 emb CAD32599.1 </u>	unnamed protein product [Drosop...	<u>21</u>	63
<u>gi 14112251 gb AAE57668.1 </u>	Sequence 40 from patent US 6177075	<u>21</u>	63
<u>gi 11191607 emb CAC16344.1 </u>	unnamed protein product [uniden...	<u>21</u>	63
<u>gi 12807910 gb AAE43130.1 </u>	Sequence 2 from patent US 6074840	<u>21</u>	63
<u>gi 14118419 gb AAE59658.1 </u>	Sequence 86 from patent US 6187548	<u>21</u>	63
<u>gi 16236295 gb AAE78102.1 </u>	Sequence 9 from patent US 627098...	<u>21</u>	63
<u>gi 270588 gb AAA02097.1 </u>	Sequence 2 from Patent US 4879374	<u>21</u>	63
<u>gi 14118420 gb AAE59659.1 </u>	Sequence 88 from patent US 6187548	<u>21</u>	63
<u>gi 3992185 gb AAC85612.1 AR004027</u>	Sequence 2 from patent US...	<u>21</u>	63
<u>gi 15124758 gb AAE73219.1 </u>	Sequence 84 from patent US 6239270	<u>21</u>	63
<u>gi 6733930 emb CAB69362.1 </u>	unnamed protein product [unident...	<u>21</u>	63
<u>gi 10184354 emb CAC08900.1 </u>	fusion between Aequorea victori...	<u>21</u>	63
<u>gi 14118418 gb AAE59657.1 </u>	Sequence 84 from patent US 6187548	<u>21</u>	63
<u>gi 21899919 emb CAD42378.1 </u>	unnamed protein product [Homo s...	<u>21</u>	63
<u>gi 1830486 gb AAB44940.1 </u>	Sequence 29 from patent US 558745...	<u>21</u>	84
<u>gi 15121888 gb AAE72568.1 </u>	Sequence 4 from patent US 6236946	<u>21</u>	84
<u>gi 1831302 gb AAB45756.1 </u>	Sequence 3 from patent US 5591821	<u>21</u>	84
<u>gi 1611873 gb AAB14852.1 </u>	Sequence 5 from patent US 5541311...	<u>21</u>	84
<u>gi 592412 gb AAA54019.1 </u>	Sequence 2 from Patent WO 8905355 ...	<u>21</u>	84
<u>gi 10063187 gb AAE38127.1 </u>	Sequence 16 from patent US 5993827	<u>21</u>	84
<u>gi 1831307 gb AAB45761.1 </u>	Sequence 13 from patent US 5591821	<u>21</u>	84
<u>gi 15864475 emb CAC88676.1 </u>	unnamed protein product [Homo s...	<u>21</u>	84
<u>gi 21438922 emb CAD34848.1 </u>	unnamed protein product [Homo s...	<u>21</u>	84

### Alignments

Get selected sequences  
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>gi|14107109|gb|AAE55963.1| Sequence 5 from patent US 6165469  
gi|14107110|gb|AAE55964.1| Sequence 6 from patent US 6165469  
gi|14118261|gb|AAE59500.1| Sequence 5 from patent US 6187310  
 Length = 1292

Score = 27.4 bits (57), Expect = 0.76  
 Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KCV  
 Sbjct: 730 DDCNSRKSQCGNFNGKCV 747

>gi|14118262|gb|AAE59501.1| Sequence 6 from patent US 6187310  
 Length = 1277

Score = 27.4 bits (57), Expect = 0.76  
 Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KCV  
 Sbjct: 715 DDCNSRKSQCGNFNGKCV 732

>gi|14118260|gb|AAE59499.1| Sequence 3 from patent US 6187310

Length = 1276

Score = 25.2 bits (52), Expect = 3.3  
Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
DDC SRK C FN KC+  
Sbjct: 714 DDCNSRKSQCGNFNGKCI 731

>gi|14107107|gb|AAE55961.1| Sequence 2 from patent US 6165469  
Length = 1295

Score = 25.2 bits (52), Expect = 3.3  
Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
DDC SRK C FN KC+  
Sbjct: 729 DDCNSRKSQCGNFNGKCI 746

>gi|14107108|gb|AAE55962.1| Sequence 3 from patent US 6165469  
gi|14118259|gb|AAE59498.1| Sequence 2 from patent US 6187310  
Length = 1291

Score = 25.2 bits (52), Expect = 3.3  
Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
DDC SRK C FN KC+  
Sbjct: 729 DDCNSRKSQCGNFNGKCI 746

>gi|20268211|gb|AAM17448.1| Sequence 29 from patent US 6361964  
Length = 469

Score = 24.8 bits (51), Expect = 4.4  
Identities = 12/28 (42%), Positives = 15/28 (53%), Gaps = 12/28 (42%)

Query: 6 QKCF-Q---HLDDCCSRKC-----NRFN 24  
Q+CF Q +LDDC C +RFN  
Sbjct: 33 QRCFCQVSGYLDCC---TCDVETIDRFN 57

>gi|15797474|emb|CAC88318.1| unnamed protein product [Homo sapiens]  
Length = 596

Score = 24.8 bits (51), Expect = 4.4  
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 8 CFQHLDDC 15  
CFQ LDDC  
Sbjct: 253 CFQILDDC 260

>gi|21715796|emb|CAD38256.1| unnamed protein product [Homo sapiens]

Length = 537

Score = 24.8 bits (51), Expect = 4.4  
Identities = 10/19 (52%), Positives = 11/19 (57%), Gaps = 5/19 (26%)

Query: 11 HLDDCCS-----RKCNRFN 24  
      HL D S           RKC+RFN  
Sbjct: 412 HLGDGSSDLILIRKCSRNFN 430

>gi|21886477|emb|CAD42152.1|    unnamed protein product [Homo sapiens]  
Length = 377

Score = 24.4 bits (50), Expect = 6.0  
Identities = 8/11 (72%), Positives = 8/11 (72%)

Query: 12 LDDCCSRKCNR 22  
      LDDC SR C R  
Sbjct: 207 LDDCASRPCQR 217

Score = 18.9 bits (37), Expect = 272  
Identities = 6/10 (60%), Positives = 7/10 (70%), Gaps = 1/10 (10%)

Query: 13 DDCCSRKCNR 22  
      DDC S C+R  
Sbjct: 27 DDCSSH-CDR 35

>gi|2302756|emb|CAA03163.1|    unnamed protein product [Eimeria maxima]  
gi|10067156|gb|AAE40146.1|    Sequence 2 from patent US 6001363  
Length = 109

Score = 24.0 bits (49), Expect = 8.0  
Identities = 10/19 (52%), Positives = 10/19 (52%), Gaps = 9/19 (47%)

Query: 7 KCFQHLDDCCSRK--CNRF 23  
      KC           CCS K CNRF  
Sbjct: 52 KC-----CCS-KFCCNRF 63

Score = 17.6 bits (34), Expect = 658  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 15 CCSR 18  
      CCSR  
Sbjct: 68 CCSR 71

Score = 16.3 bits (31), Expect = 1589  
Identities = 4/6 (66%), Positives = 4/6 (66%)

Query: 15 CCSRKC 20  
      CC KC  
Sbjct: 33 CCCSKC 38

Score = 16.3 bits (31), Expect = 1589  
Identities = 4/6 (66%), Positives = 4/6 (66%)

Query: 15 CCSRKC 20  
CC KC  
Sbjct: 28 CCCSKC 33

>gi|16243883|gb|AAE80395.1| Sequence 8 from patent US 6284253  
Length = 498

Score = 24.0 bits (49), Expect = 8.0  
Identities = 15/34 (44%), Positives = 16/34 (47%), Gaps = 12/34 (35%)

Query: 2 RIPNQ--KCFQ----HLD-DC-CSRKCNRFNKC 26  
R P Q KCF HL +C RKC NKC  
Sbjct: 403 RRPQQLKCFNCGKPGHLARNCRAPRKC---NKC 433

>gi|4530797|emb|CAA03824.1| unnamed protein product [unidentified]  
gi|4530807|emb|CAA03828.1| unnamed protein product [unidentified]  
Length = 95

Score = 23.5 bits (48), Expect = 11  
Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKCV 27  
CF+HLD +C KC N + +KCV  
Sbjct: 20 CFRHLDEREEC---KCLLN-YKQEGDKCV 44

>gi|3409411|gb|AAC30466.1|I89471| Sequence 1 from patent US 5720959  
Length = 48

Score = 23.5 bits (48), Expect = 11  
Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKCV 27  
CF+HLD +C KC N + +KCV  
Sbjct: 18 CFRHLDEREEC---KCLLN-YKQEGDKCV 42

>gi|4530805|emb|CAA03827.1| unnamed protein product [unidentified]  
gi|4530815|emb|CAA03831.1| unnamed protein product [unidentified]  
Length = 108

Score = 23.5 bits (48), Expect = 11  
Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKCV 27  
CF+HLD +C KC N + +KCV  
Sbjct: 33 CFRHLDEREEC---KCLLN-YKQEGDKCV 57

>gi|3999143|gb|AAC92575.1|AR021637 Sequence 3 from patent US 5789198  
 Length = 145

Score = 23.5 bits (48), Expect = 11  
 Identities = 10/19 (52%), Positives = 10/19 (52%), Gaps = 5/19 (26%)

Query: 1 CRIPNQKCFQHLDCCSRK 19  
 C I Q CF DCCS K  
 Sbjct: 3 CHIHIQ-CF----DCCSMK 16

>gi|4530800|emb|CAA03825.1| unnamed protein product [unidentified]  
gi|4530810|emb|CAA03829.1| unnamed protein product [unidentified]  
 Length = 116

Score = 23.5 bits (48), Expect = 11  
 Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKCV 27  
 CF+HLD +C KC N + +KCV  
 Sbjct: 20 CFRHLDEREEC---KCLLN-YKQEGDKCV 44

>gi|3409412|gb|AAC30467.1|I89472 Sequence 2 from patent US 5720959  
 Length = 48

Score = 23.5 bits (48), Expect = 11  
 Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKCV 27  
 CF+HLD +C KC N + +KCV  
 Sbjct: 18 CFRHLDEREEC---KCLLN-YKQEGDKCV 42

>gi|3409416|gb|AAC30471.1|I89476 Sequence 12 from patent US 5720959  
 Length = 48

Score = 23.5 bits (48), Expect = 11  
 Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKCV 27  
 CF+HLD +C KC N + +KCV  
 Sbjct: 18 CFRHLDEREEC---KCLLN-YKQEGDKCV 42

>gi|4530803|emb|CAA03826.1| unnamed protein product [unidentified]  
gi|4530813|emb|CAA03830.1| unnamed protein product [unidentified]  
 Length = 127

Score = 23.5 bits (48), Expect = 11  
 Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKCV 27  
 CF+HLD +C KC N + +KCV  
 Sbjct: 52 CFRHLDEREEC---KCLLN-YKQEGDKCV 76

>gi|20221551|gb|AAE87124.1| Sequence 11 from patent US 6326165  
Length = 716

Score = 23.1 bits (47), Expect = 14  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CFQHLDD 14  
CF HLDD  
Sbjct: 439 CFMHLDD 445

>gi|12822272|gb|AAE48713.1| Sequence 6 from patent US 6107088  
Length = 178

Score = 23.1 bits (47), Expect = 14  
Identities = 7/14 (50%), Positives = 8/14 (57%)

Query: 3 IPNQKCFQHLDCC 16  
IP K F H+ CC  
Sbjct: 160 IPENKYFHHMGKCC 173

>gi|20221546|gb|AAE87119.1| Sequence 4 from patent US 6326165  
Length = 737

Score = 23.1 bits (47), Expect = 14  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CFQHLDD 14  
CF HLDD  
Sbjct: 460 CFMHLDD 466

>gi|12822270|gb|AAE48711.1| Sequence 2 from patent US 6107088  
Length = 317

Score = 23.1 bits (47), Expect = 14  
Identities = 7/14 (50%), Positives = 8/14 (57%)

Query: 3 IPNQKCFQHLDCC 16  
IP K F H+ CC  
Sbjct: 160 IPENKYFHHMGKCC 173

>gi|20221547|gb|AAE87120.1| Sequence 5 from patent US 6326165  
Length = 716

Score = 23.1 bits (47), Expect = 14  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CFQHLDD 14  
CF HLDD  
Sbjct: 439 CFMHLDD 445

>gi|16242616|gb|AAE79920.1| Sequence 20 from patent US 6280975  
Length = 13

Score = 22.7 bits (46), Expect = 19  
Identities = 5/7 (71%), Positives = 7/7 (100%)

Query: 20 CNRFNKC 26  
C++FNKC  
Sbjct: 2 CDKFNKC 8

>gi|410755|emb|CAA00367.1| P.195 [Plasmodium falciparum]  
Length = 1654

Score = 22.7 bits (46), Expect = 19  
Identities = 8/16 (50%), Positives = 10/16 (62%), Gaps = 6/16 (37%)

Query: 8 CFQHLD---DCCSRKC 20  
CF+HLD +C KC  
Sbjct: 1558 CFRHLDERECC---KC 1570

Score = 16.8 bits (32), Expect = 1184  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 22 RFNK 25  
RFNK  
Sbjct: 1332 RFNK 1335

>gi|15118603|gb|AAE70697.1| Sequence 100 from patent US 6232061  
Length = 520

Score = 22.3 bits (45), Expect = 26  
Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 2/10 (20%)

Query: 8 CFQH--LDDC 15  
CFQH LD C  
Sbjct: 317 CFQHMILDTC 326

>gi|23330539|gb|AAN26530.1| Sequence 2 from patent US 6432408  
Length = 1708

Score = 22.3 bits (45), Expect = 26  
Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 3/10 (30%)

Query: 12 LDD---CCSR 18  
LDD CCSR  
Sbjct: 330 LDDQAFCCSR 339

>gi|15141755|emb|CAC50180.1| Orf1 [Hepatitis E virus]  
Length = 1698

Score = 22.3 bits (45), Expect = 26  
 Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 3/10 (30%)

Query: 12 LDD---CCSR 18  
 LDD CCSR  
 Sbjct: 321 LDDQAFCCSR 330

>gi|1254372|gb|AAA95626.1| Sequence 6 from patent US 5482928  
gi|3012065|gb|AAC11513.1|I75924 Sequence 6 from patent US 5689048  
 Length = 25

Score = 22.3 bits (45), Expect = 26  
 Identities = 8/13 (61%), Positives = 9/13 (69%), Gaps = 1/13 (7%)

Query: 14 DCCSRKCNRFNKC 26  
 DCC+ CNR KC  
 Sbjct: 14 DCCTGSCNR-GKC 25

>gi|20227333|gb|AAE89374.1| Sequence 36 from patent US 6340740  
gi|23330622|gb|AAN26602.1| Sequence 31 from patent US 6432628  
 Length = 47

Score = 22.3 bits (45), Expect = 26  
 Identities = 7/16 (43%), Positives = 9/16 (56%), Gaps = 7/16 (43%)

Query: 7 KCFQHL-----DDC 15  
 KCFQ+L +DC  
 Sbjct: 18 KCFQNLGFEVTVHNDC 33

>gi|3209904|gb|AAC20848.1|I81607 Sequence 2 from patent US 5710019  
 Length = 513

Score = 22.3 bits (45), Expect = 26  
 Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 11 HLDDCCSR 18  
 HLD CC R  
 Sbjct: 160 HLDGCCKR 167

>gi|3991599|gb|AAC85026.1|AR002030 Sequence 52 from patent US 5739281  
 Length = 4544

Score = 22.3 bits (45), Expect = 26  
 Identities = 10/19 (52%), Positives = 13/19 (68%), Gaps = 5/19 (26%)

Query: 11 HLDDCCSRKC--NRFN-KC 26  
 HL CS+KC N+F+ KC  
 Sbjct: 1230 HLK--CSQKCDQNKFSVKC 1246

Score = 20.2 bits (40), Expect = 113  
 Identities = 11/26 (42%), Positives = 14/26 (53%), Gaps = 7/26 (26%)

Query: 1 CRIPNQKCFQHLDCCSRKCNRFNKC 26  
 CR NQ+C L S +CN F+ C  
 Sbjct: 3749 CR--NQRC---L--SSSLRCNMFDDC 3767

Score = 17.2 bits (33), Expect = 883  
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 21 NRFN 24  
 NRFN  
 Sbjct: 443 NRFN 446

Score = 14.6 bits (27), Expect = 5150  
 Identities = 3/4 (75%), Positives = 4/4 (100%)

Query: 12 LDCC 15  
 LD+C  
 Sbjct: 2339 LDEC 2342

Score = 13.4 bits (24), Expect = 12442  
 Identities = 4/5 (80%), Positives = 4/5 (80%)

Query: 17 SRKCN 21  
 SR CN  
 Sbjct: 89 SRLCN 93

>gi|15116726|gb|AAE70252.1| Sequence 7 from patent US 6229005  
 gi|21508670|gb|AAM58155.1| Sequence 7 from patent US 6379891  
 Length = 1693

Score = 22.3 bits (45), Expect = 26  
 Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 3/10 (30%)

Query: 12 LDD---CCSR 18  
 LDD CCSR  
 Sbjct: 330 LDDQAFCCSR 339

>gi|14484312|gb|AAE63497.1| Sequence 1 from patent US 6207416  
 gi|17905611|gb|AAE80914.1| Sequence 1 from patent US 6287759  
 Length = 1693

Score = 22.3 bits (45), Expect = 26  
 Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 3/10 (30%)

Query: 12 LDD---CCSR 18  
 LDD CCSR  
 Sbjct: 330 LDDQAFCCSR 339

>gi|1613525|gb|AAB16505.1| Sequence 2 from patent US 5559095

gi|1830459|gb|AAB44913.1| Sequence 2 from patent US 5587454  
 gi|4000574|gb|AAC94006.1|AR024748 Sequence 2 from patent US 5795864  
 gi|5942569|gb|AAE02101.1| Sequence 2 from patent US 5859186  
 gi|5972562|gb|AAE12453.1| Sequence 2 from patent US 5824645  
 gi|7223963|gb|AAE24130.1| Sequence 2 from patent US 5891849  
 gi|10054011|gb|AAE30918.1| Sequence 2 from patent US 5965534  
 gi|10064284|gb|AAE38708.1| Sequence 2 from patent US 5994305  
 gi|12815626|gb|AAE45435.1| Sequence 2 from patent US 6087091  
 gi|14477864|gb|AAE61427.1| Sequence 2 from patent US 6136786  
 Length = 25

Score = 22.3 bits (45), Expect = 26  
 Identities = 8/13 (61%), Positives = 9/13 (69%), Gaps = 1/13 (7%)

Query: 14 DCCSRKCNRFNKC 26  
 DCC+ CNR KC  
 Sbjct: 14 DCCTGSCNR-GKC 25

>gi|1613542|gb|AAB16522.1| Sequence 19 from patent US 5559095  
 gi|1830476|gb|AAB44930.1| Sequence 19 from patent US 5587454  
 gi|4000591|gb|AAC94023.1|AR024765 Sequence 19 from patent US 5795864  
 gi|5942586|gb|AAE02118.1| Sequence 19 from patent US 5859186  
 gi|5972579|gb|AAE12470.1| Sequence 19 from patent US 5824645  
 gi|7223980|gb|AAE24147.1| Sequence 19 from patent US 5891849  
 gi|10064318|gb|AAE38725.1| Sequence 19 from patent US 5994305  
 gi|12815643|gb|AAE45452.1| Sequence 19 from patent US 6087091  
 gi|14477881|gb|AAE61444.1| Sequence 19 from patent US 6136786  
 Length = 26

Score = 21.8 bits (44), Expect = 35  
 Identities = 8/13 (61%), Positives = 8/13 (61%)

Query: 14 DCCSRKCNRFNKC 26  
 DCCS C R KC  
 Sbjct: 14 DCCSGSCGRSGKC 26

>gi|1613531|gb|AAB16511.1| Sequence 8 from patent US 5559095  
 gi|1830465|gb|AAB44919.1| Sequence 8 from patent US 5587454  
 gi|4000580|gb|AAC94012.1|AR024754 Sequence 8 from patent US 5795864  
 gi|5942575|gb|AAE02107.1| Sequence 8 from patent US 5859186  
 gi|5972568|gb|AAE12459.1| Sequence 8 from patent US 5824645  
 gi|7223969|gb|AAE24136.1| Sequence 8 from patent US 5891849  
 gi|10064296|gb|AAE38714.1| Sequence 8 from patent US 5994305  
 gi|12815632|gb|AAE45441.1| Sequence 8 from patent US 6087091  
 gi|14477870|gb|AAE61433.1| Sequence 8 from patent US 6136786  
 Length = 26

Score = 21.8 bits (44), Expect = 35  
 Identities = 8/13 (61%), Positives = 8/13 (61%)

Query: 14 DCCSRKCNRFNKC 26  
 DCCS C R KC  
 Sbjct: 14 DCCSGSCGRSGKC 26

>gi|14092871|gb|AAE51612.1| Sequence 4 from patent US 6130039

gi|18093808|emb|CAD20397.1| unnamed protein product [Homo sapiens]  
 Length = 727

Score = 21.8 bits (44), Expect = 35  
 Identities = 7/13 (53%), Positives = 8/13 (61%), Gaps = 5/13 (38%)

Query: 1 CRIPNQKCFQHLD 13  
 CRI FQ+LD  
 Sbjct: 204 CRI-----FQNLD 211

>gi|4000083|gb|AAC93515.1|AR023217 Sequence 55 from patent US 5792846  
gi|59999999|gb|AAE21903.1| Sequence 55 from patent US 5851824  
 Length = 1079

Score = 21.4 bits (43), Expect = 47  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 8 CFQHL 12  
 CFQHL  
 Sbjct: 303 CFQHL 307

>gi|7224006|gb|AAE24173.1| Sequence 2 from patent US 5891857  
gi|14101230|gb|AAE53547.1| Sequence 2 from patent US 6149903  
gi|14112621|gb|AAE58038.1| Sequence 2 from patent US 6177410  
gi|20229343|gb|AAE90486.1| Sequence 49 from patent US 6342483  
 Length = 1863

Score = 21.4 bits (43), Expect = 47  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 8 CFQHL 12  
 CFQHL  
 Sbjct: 1225 CFQHL 1229

Score = 16.8 bits (32), Expect = 1184  
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 24 NKCV 27  
 NKCV  
 Sbjct: 799 NKCV 802

>gi|23342653|emb|CAD48690.1| unnamed protein product [Homo sapiens]  
gi|23342655|emb|CAD48691.1| unnamed protein product [Homo sapiens]  
gi|23342659|emb|CAD48693.1| unnamed protein product [Homo sapiens]  
 Length = 457

Score = 21.4 bits (43), Expect = 47  
 Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 3 IPNQKCFQHL 12  
 IP QKC HL  
 Sbjct: 291 IPEQKCNPHL 300

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>gi|5946864|gb|AAE03769.1| Sequence 20 from patent US 5866542
gi|5947165|gb|AAE04070.1| Sequence 20 from patent US 5866543
gi|5954014|gb|AAE06518.1| Sequence 20 from patent US 5872098
gi|10050408|gb|AAE27315.1| Sequence 20 from patent US 5955294
gi|12816345|gb|AAE46154.1| Sequence 20 from patent US 6087487
Length = 100

```

Score = 21.4 bits (43), Expect = 47  
 Identities = 8/15 (53%), Positives = 8/15 (53%), Gaps = 5/15 (33%)

Query: 12 LDDC----CSRKCN 21  
 LDDC C KCN  
 Sbjct: 35 LDDCGTQKPCEAKCN 49

```

>gi|4000084|gb|AAC93516.1|AR023218 Sequence 56 from patent US 5792846
gi|6000000|gb|AAE21904.1| Sequence 56 from patent US 5851824
Length = 1084

```

Score = 21.4 bits (43), Expect = 47  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 8 CFQHL 12  
 CFQHL  
 Sbjct: 303 CFQHL 307

```

>gi|3209905|gb|AAC20849.1|I81608 Sequence 4 from patent US 5710019
Length = 494

```

Score = 21.4 bits (43), Expect = 47  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 123 LDDCC 127

```

>gi|14100343|gb|AAE53483.1| Sequence 4 from patent US 6140485
Length = 1091

```

Score = 21.4 bits (43), Expect = 47  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 8 CFQHL 12  
 CFQHL  
 Sbjct: 303 CFQHL 307

```

>gi|5946896|gb|AAE03801.1| Sequence 62 from patent US 5866542
gi|5947197|gb|AAE04102.1| Sequence 62 from patent US 5866543
gi|5954046|gb|AAE06550.1| Sequence 62 from patent US 5872098
gi|10050440|gb|AAE27347.1| Sequence 62 from patent US 5955294
gi|12816377|gb|AAE46186.1| Sequence 62 from patent US 6087487
Length = 171

```

Score = 21.4 bits (43), Expect = 47  
 Identities = 7/13 (53%), Positives = 7/13 (53%), Gaps = 5/13 (38%)

Query: 14 DC----CSRKCN 21  
 DC C RKCN  
 Sbjct: 101 DCGNDKQCERKCN 113

>gi|15141758|emb|CAC50182.1| Orf1 [Hepatitis E virus]  
 Length = 1708

Score = 21.4 bits (43), Expect = 47  
 Identities = 6/10 (60%), Positives = 7/10 (70%), Gaps = 3/10 (30%)

Query: 12 LDD---CCSR 18  
 LBD CCSR  
 Sbjct: 330 LBDQAFCCSR 339

>gi|23342657|emb|CAD48692.1| unnamed protein product [Homo sapiens]  
 Length = 457

Score = 21.4 bits (43), Expect = 47  
 Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 3 IPNQKCFQHL 12  
 IP QKC HL  
 Sbjct: 291 IPEQKCNPHL 300

>gi|3014969|gb|AAC11849.1|I78815 Sequence 2 from patent US 5693473  
gi|3209867|gb|AAC20811.1|I81570 Sequence 2 from patent US 5709999  
gi|3209873|gb|AAC20817.1|I81576 Sequence 2 from patent US 5710001  
gi|3992676|gb|AAC86103.1|AR005620 Sequence 2 from patent US 5747282  
gi|3994270|gb|AAC87698.1|AR008672 Sequence 2 from patent US 5753441  
gi|14478556|gb|AAE61797.1| Sequence 2 from patent US 6162897  
 Length = 1863

Score = 21.4 bits (43), Expect = 47  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 8 CFQHL 12  
 CFQHL  
 Sbjct: 1225 CFQHL 1229

Score = 16.8 bits (32), Expect = 1184  
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 24 NKCV 27  
 NKCV  
 Sbjct: 799 NKCV 802

Select all  
Deselect all

Database: Protein sequences derived from the Patent division of  
GenBank

Posted date: Nov 25, 2002 1:06 AM

Number of letters in database: 16,453,681

Number of sequences in database: 104,350

Lambda K H  
0.355 0.288 2.12

Gapped

Lambda K H  
0.294 0.110 0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Hits to DB: 912,208

Number of Sequences: 104350

Number of extensions: 21292

Number of successful extensions: 3537

Number of sequences better than 20000.0: 3253

Number of HSP's better than 20000.0 without gapping: 3253

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3536

length of query: 27

length of database: 16,453,681

effective HSP length: 18

effective length of query: 9

effective length of database: 14,575,381

effective search space: 131178429

effective search space used: 131178429

T: 11

A: 40

X1: 14 ( 7.2 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 23 (13.6 bits)

S2: 23 (12.9 bits)

## NR Gen PVIIA Search

### BLASTP 2.2.4 [Aug-26-2002]

#### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038288080-013595-3111

#### Query=

(27 letters)

**Database:** All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,242,768 sequences; 395,571,179 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

#### Taxonomy reports

#### Distribution of 150 Blast Hits on the Query Sequence

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Score (bits)	E Value
Sequences producing significant alignments:	
gi 3891872 pdb 1KCP	3d Structure Of K-Conotoxin Pviia, A ...
gi 7519866 pir A58997	kappa-conotoxin PVIIA - cone shell (...)
gi 3891964 pdb 1AV3	Potassium Channel Blocker Kappa Conot...
gi 22002036 sp P56633 CXK7 CONPU	Kappa-conotoxin PVIIA prec...
gi 21402496 ref NP_658481.1	minC, Bacterial proteins invol...
gi 12656031 gb AAK00711.1 AF228515 1	polyprotein [Clitoria ...]
gi 17533597 ref NP_495391.1	Putative membrane protein, wit...
gi 310662 gb AAA30048.1	ETS homologue
gi 15603466 ref NP_246540.1	TagI [Pasteurella multocida] >...
gi 99609 pir S14947	2S albumin - Brazil nut >gi 17713 emb ...
gi 18571020 ref XP_095628.1	hypothetical protein XP_095628...
gi 23047878 gb ZP_00075808.1	hypothetical protein [Methano...
gi 90454 pir S01845	DNA (cytosine-5-)-methyltransferase (E...
gi 13878219 ref NP_113566.1	ribonuclease/angiogenin inhibi...

gi 2689716 gb AAC40061.1	DNA (cytosine-5)-methyltransferase	22	664
gi 7339827 gb AAF60965.1	DNA methyltransferase [Mus muscul...	22	664
gi 12002701 gb AAG43376.1 AF155874_1	putative cytosine DNA ...	22	664
gi 1765919 emb CAA32910.1	DNA methyltransferase 1 [Mus mus...	22	664
gi 6753664 ref NP_034196.1	DNA methyltransferase (cytosine...	22	664
gi 24475410 dbj BAC22660.1	plexinB1 [Mus musculus]	22	890
gi 15596236 ref NP_249730.1	conserved hypothetical protein...	21	1195
gi 7434825 pir T13810	DNA-directed DNA polymerase (EC 2.7....	21	1195
gi 1272304 gb AAB01144.1	alpha esterase	21	1195
gi 6325231 ref NP_015299.1	multicopy suppressor of snf3 an...	21	1195
gi 24585481 ref NP_610051.2	CG9316-PA [Drosophila melanoga...	21	1195
gi 24583179 ref NP_609327.2	CG31712-PA [Drosophila melanog...	21	1195
gi 23468631 gb ZP_00123966.1	hypothetical protein [Pseudom...	21	1195
gi 19527983 gb AAL90106.1	AT19096p [Drosophila melanogaster]	21	1195
gi 25032745 ref XP_206420.1	hypothetical protein XP_206420...	21	1195
gi 7661970 ref NP_055455.1	KIAA0173 gene product [Homo sap...	21	1195
gi 20070166 ref NP_002227.2	potassium voltage-gated channe...	21	1195
gi 16945371 emb CAB97275.2	conserved hypothetical protein ...	21	1195
gi 7513252 pir  JC5919	potassium channel 1 - human >gi 2739...	21	1195
gi 2494180 sp Q27607 DPG1_DROME	DNA polymerase gamma subunit	21	1195
gi 12849875 dbj BAB28515.1	Hbs1-like (S. cerevisiae)~data ...	21	1195
gi 12619543 gb AAG60433.1 AF215005_1	conotoxin scaffold VI/...	21	1195
gi 19074436 ref NP_585942.1	similarity to GCN1-LIKE TRANSL...	21	1195
gi 23475177 gb ZP_00130466.1	hypothetical protein [Desulfo...	21	1195
gi 19527699 gb AAL89964.1	AT02241p [Drosophila melanogaster]	21	1195
gi 13358405 ref NP_078748.1	hypothetical protein [Lymphocy...	21	1195
gi 16944565 emb CAC18184.2	conserved hypothetical protein ...	21	1195
gi 21288647 gb EAA00940.1	agCP12708 [Anopheles gambiae str...	21	1195
gi 11359505 pir  T50956	hypothetical protein B24P7.110 [imp...	21	1195
gi 25146207 ref NP_741523.1	Glycosyl transferase (38.8 kD)...	21	1195
gi 24644854 ref NP_524267.2	CG1257-PA [Drosophila melanoga...	21	1195
gi 7505021 pir  T34006	hypothetical protein H43I07.2 - Caen...	21	1195
gi 6478764 gb AAF13991.1 AF200581_3	coat protein [Soybean m...	21	1195
gi 22055778 ref XP_090213.5	hypothetical protein XP_090213...	21	1195
gi 21293200 gb EAA05345.1	agCP9199 [Anopheles gambiae str....	21	1195
gi 21553101 ref NP_660128.1	afamin precursor; alpha albumi...	21	1195
gi 15233602 ref NP_194676.1	putative protein; protein id: ...	21	1195
gi 17136648 ref NP_476821.1	CG8987-PA [Drosophila melanoga...	21	1195
gi 11890594 gb AAG41136.1	polyprotein [Soybean mosaic viru...	21	1195
gi 6478701 gb AAF13964.1 AF200554_2	coat protein [Soybean m...	21	1195
gi 22964283 gb ZP_00011889.1	hypothetical protein [Rhodops...	21	1195
gi 20072386 gb AAH26681.1	Unknown (protein for IMAGE:50644...	21	1195
gi 17158399 ref NP_477819.1	wsv297 [shrimp white spot synd...	21	1195
gi 20845975 ref XP_137981.1	similar to potassium voltage-g...	21	1195
gi 15616394 ref NP_244699.1	BH3832~unknown [Bacillus halod...	21	1195
gi 20090341 ref NP_616416.1	potassium uptake protein [Meth...	21	1195
gi 21295843 gb EAA07988.1	agCP1575 [Anopheles gambiae str....	21	1195
gi 1435084 emb CAA67549.1	zinc finger protein [Ascobolus i...	21	1195
gi 1438541 gb AAB04099.1	sarcoendoplasmic reticulum Ca2+ A...	21	1603
gi 1815634 gb AAC44800.1	glutamine synthetase type 1	21	1603
gi 21672065 gb AAM74427.1 AC123594_10	Putative lipid transf...	21	1603
gi 19920032 gb AAM08471.1	hypothetical protein [Dictyostel...	21	1603
gi 15224439 ref NP_181342.1	hypothetical protein; protein ...	21	1603
gi 6760665 gb AAD45537.2 AF164678_1	FLASH homolog RIP25 [Ho...	21	1603
gi 13376109 ref NP_079042.1	hypothetical protein FLJ23451 ...	21	1603
gi 17545702 ref NP_519104.1	HYPOTHETICAL PROTEIN [Ralstoni...	21	1603
gi 18584880 ref XP_102118.1	hypothetical protein XP_102118...	21	1603
gi 1905981 gb AAB50229.1	Gal/GalNAc lectin heavy subunit [...	21	1603
gi 6681641 dbj BAA88816.1	Yb-B19L [Yaba monkey tumor virus]	21	1603
gi 21233883 ref NP_640181.1	hypothetical protein [Proteus ...	21	1603
gi 18676383 emb CAD21521.1	Brachyury [Podocoryne carneal]	21	1603

gi 20521882 dbj BAA92553.2	KIAA1315 protein [Homo sapiens]	21	1603
gi 11288744 pir  T49852	hypothetical protein B24P11.80 [imp...]	21	1603
gi 16197658 emb CAC82967.1	putative transposition protein ...	21	1603
gi 13508551 emb CAC35152.1	TniB protein [Achromobacter xyl...]	21	1603
gi 20810180 gb AAH29359.1	similar to hypothetical protein ...	21	1603
gi 18397365 ref NP_566259.1	Lon protease, putative; protei...	21	1603
gi 23601348 ref XP_178510.1	hypothetical protein XP_178510...	21	1603
gi 20091070 ref NP_617145.1	predicted protein [Methanosa...	21	1603
gi 15920020 ref NP_361080.1	TniB protein [Plasmid pSB102] ...	21	1603
gi 23509421 ref NP_702088.1	hypothetical protein [Plasmodi...	21	1603
gi 15805858 ref NP_294556.1	conserved hypothetical protein...	21	1603
gi 7949131 ref NP_058025.1	ATPase, Ca++ transporting, ubiq...	21	1603
gi 21299840 gb EAA11985.1	agCP8898 [Anopheles gambiae str....	21	1603
gi 17548954 ref NP_522294.1	HYPOTHETICAL PROTEIN [Ralstoni...	21	1603
gi 6912288 ref NP_036247.1	CASP8 associated protein 2; FLI...	21	1603
gi 21291427 gb EAA03572.1	agCP14274 [Anopheles gambiae str...	21	1603
gi 20346229 ref XP_109250.1	ATPase, Ca++ transporting, ubiq...	21	1603
gi 7662376 ref NP_055698.1	KIAA0914 gene product [Homo sap...	21	1603
gi 121226 sp P13578 GLB3_TYLHE	Globin IIB, extracellular (E...	21	1603
gi 6753288 ref NP_036127.1	caspase 8 associated protein 2;...	21	1603
gi 23509386 ref NP_702053.1	hypothetical protein [Plasmodi...	21	1603
gi 7439466 pir  S71915	hemoglobin, extracellular, chain B -...	21	1603
gi 12057020 emb CAC19873.1	putative notch receptor protein...	21	1603
gi 1389559 gb AAB02882.1	glycoprotein 330	21	1603
gi 21672069 gb AAM74431.1 AC123594 14	Putative lipid tranfe...	21	1603

### Alignments

Get selected sequences  
 Select all  
 Deselect all

>gi|3891872|pdb|1KCP| 3d Structure Of K-Conotoxin Pviia, A Novel Potassium Channel-Blocking Toxin From Cone Snails, Nmr, 22 Structures Length = 28

Score = 45.2 bits (99), Expect = 8e-05  
 Identities = 19/27 (70%), Positives = 19/27 (70%)

Query: 1 CXIXNQXCXQHLDCCSXXCNXXNCV 27  
 C I NQ C QHLDCCS CN N CV  
 Sbjct: 1 CRIXNQKCFQHLDCCSRKCNRFNKCV 27

>gi|7519866|pir||A58997 kappa-conotoxin PVIIA - cone shell (Conus purpurascens)  
 Length = 27

Score = 45.2 bits (99), Expect = 8e-05  
 Identities = 18/27 (66%), Positives = 18/27 (66%)

Query: 1 CXIXNQXCXQHLDCCSXXCNXXNCV 27  
 C I NQ C QHLDCCS CN N CV  
 Sbjct: 1 CRIPNQKCFQHLDCCSRKCNRFNKCV 27

>gi|3891964|pdb|1AV3| Potassium Channel Blocker Kappa Conotoxin Pviiia From C. Purpurascens, Nmr, 20 Structures  
Length = 27

Score = 45.2 bits (99), Expect = 8e-05  
Identities = 19/27 (70%), Positives = 19/27 (70%)

Query: 1 CXIXNQXCXQHLDCCSXXCNXXNCV 27  
C I NQ C QHLDCCS CN N CV  
Sbjct: 1 CRIXNQKCFQHLDCCSRKCNRFNKC 27

>gi|22002036|sp|P56633|C XK7 CONPU Kappa-conotoxin PVIIA precursor (Fin-popping peptide)  
Length = 72

Score = 45.2 bits (99), Expect = 8e-05  
Identities = 18/27 (66%), Positives = 18/27 (66%)

Query: 1 CXIXNQXCXQHLDCCSXXCNXXNCV 27  
C I NQ C QHLDCCS CN N CV  
Sbjct: 46 CRIPNQKCFQHLDCCSRKCNRFNKC 72

>gi|21402496|ref|NP\_658481.1| minC, Bacterial proteins involved in chromosomal partitioning  
[Bacillus anthracis A2012]  
Length = 228

Score = 27.8 bits (58), Expect = 15  
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 11 HLDDCCS 17  
HLDDCCS  
Sbjct: 21 HLDDCCS 27

>gi|12656031|gb|AAK00711.1|AF228515 1 polyprotein [Clitoria virus Y]  
Length = 489

Score = 23.5 bits (48), Expect = 275  
Identities = 6/9 (66%), Positives = 7/9 (77%)

Query: 8 CXQHLDCC 16  
C QH+D CC  
Sbjct: 197 CAQHIDGCC 205

>gi|17533597|ref|NP\_495391.1| Putative membrane protein, with at least 2 transmembrane domains  
[Caenorhabditis elegans]  
gi|7500246|pir||T16223 hypothetical protein F31E8.4 - Caenorhabditis elegans  
gi|1280155|gb|AAA98020.1| Hypothetical protein F31E8.4 [Caenorhabditis elegans]  
Length = 162

Score = 23.1 bits (47), Expect = 369  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 10 QHLDCC 16  
QHL DCC  
Sbjct: 156 QHLTDCC 162

>gi|310662|gb|AAA30048.1| ETS homologue  
Length = 559  
  
Score = 22.7 bits (46), Expect = 495  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 11 HLDDCC 16  
HLD+CC  
Sbjct: 22 HLDECC 27

>gi|15603466|ref|NP\_246540.1| TagI [Pasteurella multocida]  
gi|12721997|gb|AAK03685.1| TagI [Pasteurella multocida]  
Length = 183  
  
Score = 22.7 bits (46), Expect = 495  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 11 HLDDCC 16  
HL+DCC  
Sbjct: 176 HLNDCC 181

>gi|99609|pir||S14947 2S albumin - Brazil nut  
gi|17713|emb|CAA38363.1| 2S albumin [Bertholletia excelsa]  
Length = 154  
  
Score = 22.7 bits (46), Expect = 495  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 11 HLDDCC 16  
HLD+CC  
Sbjct: 86 HLDECC 91

>gi|18571020|ref|XP\_095628.1| hypothetical protein XP\_095628 [Homo sapiens]  
Length = 276  
  
Score = 22.7 bits (46), Expect = 495  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 11 HLDDCCS 17  
HL DCCS  
Sbjct: 99 HLKDCCS 105

>gi|23047878|gb|ZP\_00075808.1| hypothetical protein [Methanosaarcina barkeri]  
Length = 175  
  
Score = 22.3 bits (45), Expect = 664  
Identities = 5/7 (71%), Positives = 7/7 (100%)

Query: 10 QHLDCC 16  
Q+LD+CC  
Sbjct: 155 QNLDECC 161

>gi|90454|pir||S01845 DNA (cytosine-5)-methyltransferase (EC 2.1.1.37) - mouse  
Length = 1573

Score = 22.3 bits (45), Expect = 664  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
C QHLDD  
Sbjct: 242 CGQHLDD 248

>gi|13878219|ref|NP\_113566.1| ribonuclease/angiogenin inhibitor 2 [Mus musculus]  
gi|13603845|gb|AAK31960.1|AF285581\_1| ribonuclease/angiogenin inhibitor 2 [Mus  
musculus]  
Length = 748

Score = 22.3 bits (45), Expect = 664  
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 1/11 (9%)

Query: 3 IXNQXCXQHLD 13  
I NQ C QHLD  
Sbjct: 453 IQNQ-CLQHLD 462

>gi|2689716|gb|AAC40061.1| DNA (cytosine-5)-methyltransferase [Mus musculus]  
Length = 1502

Score = 22.3 bits (45), Expect = 664  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
C QHLDD  
Sbjct: 243 CGQHLDD 249

>gi|7339827|gb|AAF60965.1| DNA methyltransferase [Mus musculus]  
gi|9719249|gb|AAF97695.1| DNA (cytosine-5)-methyltransferase [Mus musculus]  
Length = 1502

Score = 22.3 bits (45), Expect = 664  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
C QHLDD  
Sbjct: 244 CGQHLDD 250

>gi|12002701|gb|AAG43376.1|AF155874\_1| putative cytosine DNA methyltransferase [Oryza  
sativa]  
Length = 1501

Score = 22.3 bits (45), Expect = 664  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
 C QHLDD  
 Sbjct: 243 CGQHLDD 249

>gi|1765919|emb|CAA32910.1| DNA methyltransferase 1 [Mus musculus]  
 Length = 1620

Score = 22.3 bits (45), Expect = 664  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
 C QHLDD  
 Sbjct: 361 CGQHLDD 367

>gi|6753664|ref|NP\_034196.1| DNA methyltransferase (cytosine-5) [Mus musculus]  
gi|20141336|sp|P13864|DNM1\_MOUSE DNA (cytosine-5)-methyltransferase 1 (Dnmt1) (DNA  
 methyltransferase  
 MmuI) (DNA MTase MmuI) (MCMT) (M.MmuI) (Met-1)  
gi|6625687|gb|AAF19352.1| DNA methyltransferase [Mus musculus]  
 Length = 1620

Score = 22.3 bits (45), Expect = 664  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
 C QHLDD  
 Sbjct: 362 CGQHLDD 368

>gi|24475410|dbj|BAC22660.1| plexinB1 [Mus musculus]  
 Length = 2119

Score = 21.8 bits (44), Expect = 890  
 Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 1/10 (10%)

Query: 8 CXQHLD-DCC 16  
 C QHLD D C  
 Sbjct: 482 CAQHLD\_CDSC 491

>gi|15596236|ref|NP\_249730.1| conserved hypothetical protein [Pseudomonas aeruginosa  
 PA01]  
gi|11347735|pir||G83515 conserved hypothetical protein PA1039 [imported] - Pseudomonas  
 aeruginosa (strain PA01)  
gi|9946952|gb|AAG04428.1|AE004536\_7 conserved hypothetical protein [Pseudomonas  
 aeruginosa PA01]  
 Length = 157

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 14 LDDCC 18

>gi|7434825|pir||T13810 DNA-directed DNA polymerase (EC 2.7.7.7) gamma, mitochondrial -  
 fruit fly (*Drosophila melanogaster*)  
gi|2289912|gb|AAC47658.1| mitochondrial DNA polymerase catalytic subunit precursor  
 [Drosophila melanogaster]  
 Length = 1145

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 662 LDDCC 666

>gi|1272304|gb|AAB01144.1| alpha esterase  
 Length = 548

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 10 QHLDDC 15  
 +HLDCC  
 Sbjct: 273 EHLDCC 278

>gi|6325231|ref|NP\_015299.1| multicopy suppressor of snf3 and grr1 mutants; Sks1p  
 [Saccharomyces  
 cerevisiae]  
gi|2499625|sp|Q12505|SKS1 YEAST Serine/threonine-protein kinase SKS1 (Suppressor  
 kinase of SNF3)  
gi|2133138|pir||S61935 SKS1 protein - yeast (Saccharomyces cerevisiae)  
gi|1039451|gb|AAB68161.1| Sha3p  
gi|1173541|gb|AAC49570.1| Sks1p  
 Length = 502

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/7 (71%), Positives = 7/7 (100%)

Query: 11 HLDDCCS 17  
 H+D+CCS  
 Sbjct: 243 HVDECCS 249

>gi|24585481|ref|NP\_610051.2| CG9316-PA [Drosophila melanogaster]  
gi|22946930|gb|AAF53915.2| CG9316-PA [Drosophila melanogaster]  
 Length = 448

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC

Sbjct: 236 LDDCC 240

>gi|24583179|ref|NP\_609327.2| CG31712-PA [Drosophila melanogaster]  
 gi|22946070|gb|AAF52833.2| CG31712-PA [Drosophila melanogaster]  
 Length = 309

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC

Sbjct: 216 LDDCC 220

>gi|23468631|gb|ZP\_00123966.1| hypothetical protein [Pseudomonas syringae pv. syringae B728a]  
 Length = 610

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC

Sbjct: 304 LDDCC 308

>gi|19527983|gb|AAL90106.1| AT19096p [Drosophila melanogaster]  
 Length = 447

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC

Sbjct: 234 LDDCC 238

>gi|25032745|ref|XP\_206420.1| hypothetical protein XP\_206420 [Mus musculus]  
 Length = 118

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 10 QHLDDC 15  
 HLDCC

Sbjct: 10 HHLDCC 15

>gi|7661970|ref|NP\_055455.1| KIAA0173 gene product [Homo sapiens]  
 gi|20455377|sp|Q14679|Y173 HUMAN Hypothetical protein KIAA0173  
 gi|1136406|dbj|BAA11490.1| similar to pig tubulin-tyrosine ligase. [Homo sapiens]  
 Length = 1199

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 12 LDDCCS 17  
 L+DCCS  
 Sbjct: 519 LEDCCS 524

>gi|20070166|ref|NP\_002227.2| potassium voltage-gated channel, subfamily F, member 1;  
 potassium  
 channel KH1 [Homo sapiens]  
 gi|24418476|sp|Q9H3M0|KCF1\_HUMAN Potassium voltage-gated channel subfamily F member 1  
 (Voltage-gated  
 potassium channel protein Kv5.1) (KH1)  
 gi|12001824|gb|AAG43055.1| potassium channel [Homo sapiens]  
 gi|19913491|gb|AAH26110.1| potassium voltage-gated channel, subfamily F, member 1  
 [Homo  
 sapiens]  
 Length = 494

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 123 LDDCC 127

>gi|16945371|emb|CAB97275.2| conserved hypothetical protein [Neurospora crassa]  
 Length = 1405

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 10 QHLDDC 15  
 +HLDDC  
 Sbjct: 1182 EHLDDC 1187

>gi|7513252|pir||JC5919 potassium channel.1 - human  
 gi|2739501|gb|AAC05597.1| potassium channel [Homo sapiens]  
 Length = 494

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 123 LDDCC 127

>gi|2494180|sp|Q27607|DPG1\_DROME DNA polymerase gamma subunit 1, mitochondrial  
 precursor  
 (Mitochondrial DNA polymerase catalytic subunit)  
 gi|7447799|pir||T13808 DNA-directed DNA polymerase (EC 2.7.7.7) gamma chain - fruit  
 fly  
 (Drosophila melanogaster)  
 gi|1401344|gb|AAC47290.1| DNA polymerase gamma  
 Length = 1145

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 662 LDDCC 666

>gi|12849875|dbj|BAB28515.1| Hbs1-like (S. cerevisiae)~data source:MGD, source  
 key:MGId:1891704,  
 evidence:ISS~putative [Mus musculus]  
 Length = 211

Score = 21.4 bits (43), Expect = 1195  
 Identities = 7/13 (53%), Positives = 7/13 (53%), Gaps = 6/13 (46%)

Query: 11 HLD-----DCCS 17  
 HLD DCCS  
 Sbjct: 163 HLDSSSKPFDCCS 175

>gi|12619543|gb|AAG60433.1|AF215005 1 conotoxin scaffold VI/VII precursor [Conus  
 ventricosus]  
 Length = 74

Score = 21.4 bits (43), Expect = 1195  
 Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 1/10 (10%)

Query: 8 CXQHLDCCS 17  
 C QH DCCS  
 Sbjct: 55 CTQH-SDCCS 63

>gi|19074436|ref|NP\_585942.1| similarity to GCN1-LIKE TRANSLATIONAL ACTIVATOR  
 [Encephalitozoon

cuniculi]

gi|19069078|emb|CAD25546.1| similarity to GCN1-LIKE TRANSLATIONAL ACTIVATOR  
 [Encephalitozoon

cuniculi]

Length = 1323

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 12 LDDCCS 17  
 LD+CCS  
 Sbjct: 779 LDECCS 784

>gi|23475177|gb|ZP\_00130466.1| hypothetical protein [Desulfovibrio desulfuricans G20]  
 Length = 589

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 10 QHLDCC 16  
 Q LD+CC

Sbjct: 203 QRLDECC 209

>gi|19527699|gb|AAL89964.1| AT02241p [Drosophila melanogaster]  
Length = 1145

Score = 21.4 bits (43), Expect = 1195  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
LDDCC

Sbjct: 662 LDDCC 666

>gi|13358405|ref|NP\_078748.1| hypothetical protein [Lymphocystis disease virus 1]  
Length = 1085

Score = 21.4 bits (43), Expect = 1195  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
LDDCC

Sbjct: 825 LDDCC 829

>gi|16944565|emb|CAC18184.2| conserved hypothetical protein [Neurospora crassa]  
Length = 590

Score = 21.4 bits (43), Expect = 1195  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 10 QHLDDC 15  
+HLDCC

Sbjct: 374 EHLDCC 379

>gi|21288647|gb|EAA00940.1| agCP12708 [Anopheles gambiae str. PEST]  
Length = 552

Score = 21.4 bits (43), Expect = 1195  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
LDDCC

Sbjct: 207 LDDCC 211

>gi|11359505|pir|T50956 hypothetical protein B24P7.110 [imported] - Neurospora crassa  
Length = 979

Score = 21.4 bits (43), Expect = 1195  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 10 QHLDDC 15  
+HLDCC

Sbjct: 756 EHLDCC 761

>gi|25146207|ref|NP\_741523.1| Glycosyl transferase (38.8 kD) [Caenorhabditis elegans]  
gi|17402836|gb|AAL38962.1|AF125965\_3| Hypothetical protein H43I07.3 [Caenorhabditis elegans]

Length = 339

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC

Sbjct: 100 LDDCC 104

>gi|24644854|ref|NP\_524267.2| CG1257-PA [Drosophila melanogaster]  
gi|17862822|gb|AAL39888.1| LP07235p [Drosophila melanogaster]  
gi|23170575|gb|AAF54004.2| CG1257-PA [Drosophila melanogaster]  
gi|25012462|gb|AAN71336.1| RE24420p [Drosophila melanogaster]

Length = 543

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 10 QHLDCC 15  
 +HLDCC

Sbjct: 273 EHLDCC 278

>gi|7505021|pir||T34006| hypothetical protein H43I07.2 - Caenorhabditis elegans  
 Length = 697

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC

Sbjct: 100 LDDCC 104

>gi|6478764|gb|AAF13991.1|AF200581\_3| coat protein [Soybean mosaic virus]  
 Length = 277

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 11 HLDDCC 16  
 H+DDCC

Sbjct: 1 HVDDCC 6

>gi|22055778|ref|XP\_090213.5| hypothetical protein XP\_090213 [Homo sapiens]  
 Length = 705

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 249 LDDCC 253

>gi|21293200|gb|EAA05345.1| agCP9199 [Anopheles gambiae str. PEST]  
 Length = 1129

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 331 LDDCC 335

>gi|21553101|ref|NP\_660128.1| afamin precursor; alpha albumin [Mus musculus]  
gi|5902744|sp|O89020|AFAM MOUSE Afamin precursor (Alpha-albumin) (Alpha-Alb)  
gi|3646361|emb|CAA09471.1| alpha-albumin protein [Mus musculus]  
 Length = 611

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 12 LDDCCS 17  
 L+DCCS  
 Sbjct: 381 LEDCCS 386

Get selected sequences  
 Select all  
 Deselect all

Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 Posted date: Nov 25, 2002 1:38 AM  
 Number of letters in database: 395,571,179  
 Number of sequences in database: 1,242,768

Lambda K H  
 0.357 0.284 2.14

Gapped  
 Lambda K H  
 0.294 0.110 0.610

Matrix: PAM30  
 Gap Penalties: Existence: 9, Extension: 1  
 Number of Hits to DB: 8,008,999  
 Number of Sequences: 1242768  
 Number of extensions: 61346  
 Number of successful extensions: 1959  
 Number of sequences better than 20000.0: 1939  
 Number of HSP's better than 20000.0 without gapping: 1939

Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1959  
length of query: 27  
length of database: 395,571,179  
effective HSP length: 18  
effective length of query: 9  
effective length of database: 373,201,355  
effective search space: 3358812195  
effective search space used: 3358812195  
T: 11  
A: 40  
X1: 14 ( 7.2 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 34 (19.3 bits)  
S2: 34 (17.6 bits)

Pat Gen PVIIA Search

**BLASTP 2.2.4 [Aug-26-2002]**

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038288110-013776-17050

**Query=**

(27 letters)

**Database:** Protein sequences derived from the Patent division of GenBank

104,350 sequences; 16,453,681 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

[Distribution of 162 Blast Hits on the Query Sequence](#)

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Score (bits)	E Value
Sequences producing significant alignments:	
gi 3209905 gb AAC20849.1 I81608	Sequence 4 from patent US 5...
gi 14118421 gb AAE59660.1	Sequence 90 from patent US 6187548
gi 14118419 gb AAE59658.1	Sequence 86 from patent US 6187548
gi 14118420 gb AAE59659.1	Sequence 88 from patent US 6187548
gi 15124758 gb AAE73219.1	Sequence 84 from patent US 6239270
gi 14118418 gb AAE59657.1	Sequence 84 from patent US 6187548
gi 5950802 gb AAE05028.1	Sequence 2 from patent US 5869282...
gi 3209904 gb AAC20848.1 I81607	Sequence 2 from patent US 5...
gi 21438796 emb CAD34785.1	unnamed protein product [Homo s...
gi 3997978 gb AAC91410.1 AR017520	Sequence 2 from patent US...
gi 18674819 emb CAD23295.1	unnamed protein product [Homo s...
gi 12824450 gb AAE49356.1	Sequence 1 from patent US 6110686
gi 15121659 gb AAE72339.1	Sequence 9 from patent US 623570...
gi 21508815 gb AAM58270.1	Sequence 1 from patent US 6379925
gi 1831307 gb AAB45761.1	Sequence 13 from patent US 5591821
	19 203

gi 1254372 gb AAA95626.1	Sequence 6 from patent US 5482928...	19	203
gi 1831303 gb AAB45757.1	Sequence 4 from patent US 5591821	19	203
gi 512010 emb CAA01442.1	ovine IL-1 beta [Ovis sp.]	19	203
gi 1613525 gb AAB16505.1	Sequence 2 from patent US 5559095...	19	203
gi 21065816 emb CAD32046.1	unnamed protein product [synthe...	19	272
gi 14110683 gb AAE57223.1	Sequence 6 from patent US 617181...	19	272
gi 4526603 emb CAA00457.1	MAb MBr1 VK sequence [synthetic ...	19	272
gi 14103731 gb AAE55165.1	Sequence 8 from patent US 6153740	19	272
gi 14103728 gb AAE55162.1	Sequence 4 from patent US 6153740	19	272
gi 14110681 gb AAE57221.1	Sequence 2 from patent US 617181...	19	272
gi 14110684 gb AAE57224.1	Sequence 7 from patent US 6171816	19	272
gi 12813715 gb AAE45015.1	Sequence 20 from patent US 6083904	19	272
gi 14103730 gb AAE55164.1	Sequence 6 from patent US 6153740	19	272
gi 14103729 gb AAE55163.1	Sequence 5 from patent US 6153740	19	272
gi 270588 gb AAA02097.1	Sequence 2 from Patent US 4879374	19	272
gi 3994136 gb AAC87564.1 AR007930	Sequence 17 from patent U...	19	272
gi 14110685 gb AAE57225.1	Sequence 8 from patent US 6171816	19	272
gi 1830486 gb AAB44940.1	Sequence 29 from patent US 558745...	18	365
gi 14119703 gb AAE60017.1	Sequence 8 from patent US 619087...	18	365
gi 3011710 gb AAC11158.1 I75569	Sequence 3 from patent US 5...	18	365
gi 1613542 gb AAB16522.1	Sequence 19 from patent US 555909...	18	365
gi 1831302 gb AAB45756.1	Sequence 3 from patent US 5591821	18	365
gi 2725130 gb AAB92812.1 I67150	Sequence 21 from patent US ...	18	365
gi 4774193 emb CAB42495.1	unnamed protein product [unident...	18	365
gi 413431 emb CAA00767.1	ORF2 [synthetic construct]	18	365
gi 10049538 gb AAE26445.1	Sequence 13 from patent US 5948900	18	365
gi 12807911 gb AAE43131.1	Sequence 4 from patent US 6074840	18	365
gi 3011709 gb AAC11157.1 I75568	Sequence 2 from patent US 5...	18	365
gi 21065678 emb CAD32037.1	unnamed protein product [Homo s...	18	365
gi 20241673 gb AAE92344.1	Sequence 338 from patent US 6348328	18	365
gi 3994135 gb AAC87563.1 AR007929	Sequence 16 from patent U...	18	365
gi 18674249 emb CAD23272.1	unnamed protein product [Homo s...	18	365
gi 3994138 gb AAC87566.1 AR007932	Sequence 19 from patent U...	18	365
gi 3011708 gb AAC11156.1 I75567	Sequence 1 from patent US 5...	18	365
gi 14097464 gb AAE52306.1	Sequence 5 from patent US 6133232	18	365
gi 20241956 gb AAE92627.1	Sequence 6 from patent US 6348348	18	365
gi 12711156 emb CAC28493.1	At position 11, R is a purine. ...	18	365
gi 1613531 gb AAB16511.1	Sequence 8 from patent US 5559095...	18	365
gi 6740790 emb CAB69452.1	ANTI FREEZE PROTEIN [Daucus carota]	18	365
gi 1830478 gb AAB44932.1	Sequence 21 from patent US 558745...	18	365
gi 1831725 gb AAB46179.1	Sequence 2 from patent US 5597707...	18	365
gi 1831305 gb AAB45759.1	Sequence 9 from patent US 5591821	18	365
gi 17915749 gb AAE84475.1	Sequence 10 from patent US 63070...	18	365
gi 3995759 gb AAC89187.1 AR013309	Sequence 3 from patent US...	18	365
gi 17915747 gb AAE84473.1	Sequence 8 from patent US 630701...	18	365
gi 5946864 gb AAE03769.1	Sequence 20 from patent US 586654...	18	490
gi 19701037 emb CAD29042.1	unnamed protein product [Homo s...	18	490
gi 5946861 gb AAE03766.1	Sequence 7 from patent US 5866542...	18	490
gi 5946859 gb AAE03764.1	Sequence 4 from patent US 5866542...	18	490
gi 16223597 gb AAE74949.1	Sequence 2 from patent US 6251655	18	658
gi 2489762 gb AAB77898.1 I59399	Sequence 4 from patent US 5...	18	658
gi 10053997 gb AAE30904.1	Sequence 3 from patent US 596552...	18	658
gi 594162 gb AAA55769.1	Sequence 17 from Patent EP 0324648	18	658
gi 10049907 gb AAE26814.1	Sequence 12 from patent US 59522...	18	658
gi 14106039 gb AAE55654.1	Sequence 23 from patent US 6160088	18	658
gi 4001198 gb AAC94630.1 AR025722	Sequence 2 from patent US...	18	658
gi 21336360 emb CAD33448.1	unnamed protein product [Homo s...	18	658
gi 23316741 gb AAN21265.1	Sequence 2 from patent US 6416734	18	658
gi 16223478 gb AAE74874.1	Sequence 2 from patent US 6251636	18	658
gi 10053996 gb AAE30903.1	Sequence 2 from patent US 596552...	18	658
gi 2484109 gb AAB72245.1 I49138	Sequence 8 from patent US 5...	18	658

<u>gi 21538090 emb CAD35982.1 </u>	prepro-PAPP-A2 coding sequence ...	<u>18</u>	658
<u>gi 12829122 gb AAE50822.1 </u>	Sequence 2 from patent US 6127159	<u>18</u>	658
<u>gi 9997807 emb CAC07548.1 </u>	unnamed protein product [Mus mus...	<u>18</u>	658
<u>gi 23329052 gb AAN25969.1 </u>	Sequence 22 from patent US 6428967	<u>18</u>	658
<u>gi 21438806 emb CAD34790.1 </u>	unnamed protein product [Homo s...	<u>18</u>	658
<u>gi 20241852 gb AAE92523.1 </u>	Sequence 517 from patent US 6348328	<u>18</u>	658
<u>gi 3211666 gb AAC21426.1 I83369</u>	Sequence 16 from patent US ...	<u>18</u>	658
<u>gi 10188331 emb CAC09134.1 </u>	unnamed protein product [Zea mays]	<u>18</u>	658
<u>gi 3999143 gb AAC92575.1 AR021637</u>	Sequence 3 from patent US...	<u>18</u>	658
<u>gi 10054000 gb AAE30907.1 </u>	Sequence 6 from patent US 596552...	<u>18</u>	658
<u>gi 23329055 gb AAN25972.1 </u>	Sequence 25 from patent US 6428967	<u>18</u>	658
<u>gi 23329053 gb AAN25970.1 </u>	Sequence 23 from patent US 6428967	<u>18</u>	658
<u>gi 3208749 gb AAC20330.1 I80459</u>	Sequence 4 from patent US 5...	<u>18</u>	658
<u>gi 10057863 gb AAE34769.1 </u>	Sequence 6 from patent US 5977442	<u>18</u>	658
<u>gi 15797474 emb CAC88318.1 </u>	unnamed protein product [Homo s...	<u>18</u>	658
<u>gi 23329054 gb AAN25971.1 </u>	Sequence 24 from patent US 6428967	<u>18</u>	658
<u>gi 6733930 emb CAB69362.1 </u>	unnamed protein product [unident...	<u>18</u>	658
<u>gi 23329051 gb AAN25968.1 </u>	Sequence 21 from patent US 6428967	<u>18</u>	658
<u>gi 3999808 gb AAC93240.1 AR022942</u>	Sequence 9 from patent US...	<u>18</u>	658
<u>gi 10049906 gb AAE26813.1 </u>	Sequence 10 from patent US 59522...	<u>18</u>	658
<u>gi 12811284 gb AAE44297.1 </u>	Sequence 5 from patent US 608054...	<u>18</u>	658
<u>gi 5953850 gb AAE06354.1 </u>	Sequence 5 from patent US 5871964...	<u>18</u>	658
<u>gi 1606923 gb AAB09880.1 </u>	Sequence 4 from patent US 5491075...	<u>17</u>	883
<u>gi 3717241 emb CAA03733.1 </u>	unnamed protein product [Senna o...	<u>17</u>	883

### Alignments

Get selected sequences  
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>gi|3209905|gb|AAC20849.1|I81608 Sequence 4 from patent US 5710019  
 Length = 494

Score = 21.4 bits (43), Expect = 47  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 123 LDDCC 127

>gi|14118421|gb|AAE59660.1| Sequence 90 from patent US 6187548  
 Length = 4655

Score = 21.0 bits (42), Expect = 63  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 11 HLDDC 15  
 HLDDC  
 Sbjct: 3096 HLDDC 3100

>gi|14118419|gb|AAE59658.1| Sequence 86 from patent US 6187548  
 Length = 4655

Score = 21.0 bits (42), Expect = 63  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 11 HLDCC 15  
HLDCC  
Sbjct: 3096 HLDCC 3100

>gi|14118420|gb|AAE59659.1| Sequence 88 from patent US 6187548  
Length = 4655

Score = 21.0 bits (42), Expect = 63  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 11 HLDCC 15  
HLDCC  
Sbjct: 3096 HLDCC 3100

>gi|15124758|gb|AAE73219.1| Sequence 84 from patent US 6239270  
Length = 4654

Score = 21.0 bits (42), Expect = 63  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 11 HLDCC 15  
HLDCC  
Sbjct: 3096 HLDCC 3100

>gi|14118418|gb|AAE59657.1| Sequence 84 from patent US 6187548  
Length = 4655

Score = 21.0 bits (42), Expect = 63  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 11 HLDCC 15  
HLDCC  
Sbjct: 3096 HLDCC 3100

>gi|5950802|gb|AAE05028.1| Sequence 2 from patent US 5869282  
>gi|10070027|gb|AAE41587.1| Sequence 2 from patent US 6004924  
Length = 1404

Score = 20.6 bits (41), Expect = 84  
Identities = 5/8 (62%), Positives = 7/8 (87%)

Query: 8 CXQHLDCC 15  
C ++LDDC  
Sbjct: 604 CAENLDDC 611

>gi|3209904|gb|AAC20848.1|I81607 Sequence 2 from patent US 5710019  
Length = 513

Score = 20.6 bits (41), Expect = 84  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 11 HLDDCC 16  
HLD CC  
Sbjct: 160 HLDGCC 165

>gi|21438796|emb|CAD34785.1| unnamed protein product [Homo sapiens]  
Length = 1105

Score = 20.2 bits (40), Expect = 113  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 10 QHLDD 14  
QHLDD  
Sbjct: 749 QHLDD 753

>gi|3997978|gb|AAC91410.1|AR017520 Sequence 2 from patent US 5777094  
Length = 1865

Score = 20.2 bits (40), Expect = 113  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 10 QHLDD 14  
QHLDD  
Sbjct: 1510 QHLDD 1514

>gi|18674819|emb|CAD23295.1| unnamed protein product [Homo sapiens]  
Length = 816

Score = 19.7 bits (39), Expect = 151  
Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
C QHLD+  
Sbjct: 110 CPQHLDE 116

>gi|12824450|gb|AAE49356.1| Sequence 1 from patent US 6110686  
Length = 178

Score = 19.7 bits (39), Expect = 151  
Identities = 6/8 (75%), Positives = 6/8 (75%), Gaps = 2/8 (25%)

Query: 10 QHL--DDC 15  
QHL DDC  
Sbjct: 125 QHLRLDDC 132

>gi|15121659|gb|AAE72339.1| Sequence 9 from patent US 6235708  
gi|16219471|gb|AAE74125.1| Sequence 9 from patent US 6245529  
Length = 145

Score = 19.7 bits (39), Expect = .151

Identities = 6/8 (75%), Positives = 6/8 (75%), Gaps = 2/8 (25%)

Query: 10 QHL--DDC 15  
QHL DDC  
Sbjct: 103 QHLRLDDC 110

>gi|21508815|gb|AAM58270.1| Sequence 1 from patent US 6379925  
Length = 1964

Score = 19.7 bits (39), Expect = 151  
Identities = 5/8 (62%), Positives = 7/8 (87%)

Query: 8 CXQHLDDC 15  
C ++LDDC  
Sbjct: 349 CEENLDDC 356

Score = 18.5 bits (36), Expect = 365  
Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 8 CXQHLDDC 15  
C Q LD+C  
Sbjct: 426 CHQDLDEC 433

>gi|1831307|gb|AAB45761.1| Sequence 13 from patent US 5591821  
Length = 29

Score = 19.3 bits (38), Expect = 203  
Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 14 DCCSXXCN 21  
+CCS CN  
Sbjct: 17 NCCSGSCN 24

>gi|1254372|gb|AAA95626.1| Sequence 6 from patent US 5482928  
gi|3012065|gb|AAC11513.1|I75924 Sequence 6 from patent US 5689048  
Length = 25

Score = 19.3 bits (38), Expect = 203  
Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 14 DCCSXXCN 21  
DCC+ CN  
Sbjct: 14 DCCTGSCN 21

>gi|1831303|gb|AAB45757.1| Sequence 4 from patent US 5591821  
Length = 25

Score = 19.3 bits (38), Expect = 203  
Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 14 DCCSXXCN 21

+CCS CN  
 Sbjct: 14 NCCSGSCN 21

>gi|512010|emb|CAA01442.1| ovine IL-1 beta [Ovis sp.]  
 Length = 266

Score = 19.3 bits (38), Expect = 203  
 Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 8 CXQHLD 13  
 C QHLD  
 Sbjct: 34 CTQHLD 39

>gi|1613525|gb|AAB16505.1| Sequence 2 from patent US 5559095  
 gi|1830459|gb|AAB44913.1| Sequence 2 from patent US 5587454  
 gi|4000574|gb|AAC94006.1|AR024748 Sequence 2 from patent US 5795864  
 gi|5942569|gb|AAE02101.1| Sequence 2 from patent US 5859186  
 gi|5972562|gb|AAE12453.1| Sequence 2 from patent US 5824645  
 gi|7223963|gb|AAE24130.1| Sequence 2 from patent US 5891849  
 gi|10054011|gb|AAE30918.1| Sequence 2 from patent US 5965534  
 gi|10064284|gb|AAE38708.1| Sequence 2 from patent US 5994305  
 gi|12815626|gb|AAE45435.1| Sequence 2 from patent US 6087091  
 gi|14477864|gb|AAE61427.1| Sequence 2 from patent US 6136786  
 Length = 25

Score = 19.3 bits (38), Expect = 203  
 Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 14 DCCSXXCN 21  
 DCC+ CN  
 Sbjct: 14 DCCTGSCN 21

>gi|21065816|emb|CAD32046.1| unnamed protein product [synthetic construct]  
 Length = 2444

Score = 18.9 bits (37), Expect = 272  
 Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 12 LDDCCSXXCN 21  
 LDDC S C+  
 Sbjct: 642 LDDCASSPCD 651

Score = 16.8 bits (32), Expect = 1184  
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 10 QHLD 13  
 QHLD  
 Sbjct: 1847 QHLD 1850

Score = 12.9 bits (23), Expect = 16694  
 Identities = 4/6 (66%), Positives = 4/6 (66%)

Query: 16 CSXXCN 21  
CS CN  
Sbjct: 1464 CSLQCN 1469

>gi|14110683|gb|AAE57223.1| Sequence 6 from patent US 6171816  
gi|15592507|emb|CAC69704.1| unnamed protein product [Homo sapiens]  
Length = 166

Score = 18.9 bits (37), Expect = 272  
Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 10 QHLDDC 15  
HL+DC  
Sbjct: 66 HHLEDC 71

>gi|4526603|emb|CAA00457.1| MAb MBr1 VK sequence [synthetic construct]  
Length = 119

Score = 18.9 bits (37), Expect = 272  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 8 CXQHLD 13  
C QHLD  
Sbjct: 98 CQQHLD 103

>gi|14103731|gb|AAE55165.1| Sequence 8 from patent US 6153740  
Length = 648

Score = 18.9 bits (37), Expect = 272  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
LD+CC  
Sbjct: 635 LDNCC 639

>gi|14103728|gb|AAE55162.1| Sequence 4 from patent US 6153740  
Length = 650

Score = 18.9 bits (37), Expect = 272  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
LD+CC  
Sbjct: 636 LDNCC 640

>gi|14110681|gb|AAE57221.1| Sequence 2 from patent US 6171816  
gi|15592501|emb|CAC69703.1| unnamed protein product [Homo sapiens]  
gi|17920557|gb|AAE86177.1| Sequence 106 from patent US 6312922  
Length = 175

Score = 18.9 bits (37), Expect = 272  
Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 10 QHLDDC 15  
HLD+C  
Sbjct: 76 HHLDEC 81

>gi|14110684|gb|AAE57224.1| Sequence 7 from patent US 6171816  
Length = 183

Score = 18.9 bits (37), Expect = 272  
Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 10 QHLDDC 15  
HL+DC  
Sbjct: 83 HHLEDC 88

>gi|12813715|gb|AAE45015.1| Sequence 20 from patent US 6083904  
Length = 2556

Score = 18.9 bits (37), Expect = 272  
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 12 LDDCCSXXCN 21  
LDDC S C+  
Sbjct: 642 LDDCASSPCD 651

Score = 16.8 bits (32), Expect = 1184  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 10 QHLD 13  
QHLD  
Sbjct: 1847 QHLD 1850

Score = 12.9 bits (23), Expect = 16694  
Identities = 4/6 (66%), Positives = 4/6 (66%)

Query: 16 CSXXCN 21  
CS CN  
Sbjct: 1464 CSLQCN 1469

>gi|14103730|gb|AAE55164.1| Sequence 6 from patent US 6153740  
Length = 649

Score = 18.9 bits (37), Expect = 272  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
LD+CC  
Sbjct: 635 LDNCC 639

>gi|14103729|gb|AAE55163.1| Sequence 5 from patent US 6153740  
Length = 649

Score = 18.9 bits (37), Expect = 272  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
LD+CC  
Sbjct: 635 LDNCC 639

>gi|270588|gb|AAA02097.1| Sequence 2 from Patent US 4879374  
Length = 266

Score = 18.9 bits (37), Expect = 272  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 8 CXQHLD 13  
C QHLD  
Sbjct: 34 CIQHLD 39

>gi|3994136|gb|AAC87564.1|AR007930 Sequence 17 from patent US 5750652  
Length = 2556

Score = 18.9 bits (37), Expect = 272  
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 12 LDDCCSXXCN 21  
LDDC S C+  
Sbjct: 642 LDDCASSPCD 651

Score = 16.8 bits (32), Expect = 1184  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 10 QHLD 13  
QHLD  
Sbjct: 1847 QHLD 1850

Score = 12.9 bits (23), Expect = 16694  
Identities = 4/6 (66%), Positives = 4/6 (66%)

Query: 16 CSXXCN 21  
CS CN  
Sbjct: 1464 CSLQCN 1469

>gi|14110685|gb|AAE57225.1| Sequence 8 from patent US 6171816  
Length = 170

Score = 18.9 bits (37), Expect = 272  
Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 10 QHLDDC 15

HL+DC

Sbjct: 70 HHLEDC 75

```
>gi|1830486|gb|AAB44940.1| Sequence 29 from patent US 5587454
gi|4000601|gb|AAC94033.1|AR024775 Sequence 29 from patent US 5795864
gi|5942596|gb|AAE02128.1| Sequence 29 from patent US 5859186
gi|5972589|gb|AAE12480.1| Sequence 29 from patent US 5824645
gi|7223990|gb|AAE24157.1| Sequence 29 from patent US 5891849
gi|10064338|gb|AAE38735.1| Sequence 29 from patent US 5994305
gi|12815653|gb|AAE45462.1| Sequence 29 from patent US 6087091
gi|14477891|gb|AAE61454.1| Sequence 29 from patent US 6136786
Length = 26
```

Score = 18.5 bits (36), Expect = 365

Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXXC 20

DCCS C

Sbjct: 14 DCCSGSC 20

```
>gi|14119703|gb|AAE60017.1| Sequence 8 from patent US 6190876
gi|20220418|gb|AAE86866.1| Sequence 8 from patent US 6319704
gi|21517011|gb|AAM60425.1| Sequence 8 from patent US 6399350
Length = 749
```

Score = 18.5 bits (36), Expect = 365

Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 13 DDCC 16

DDCC

Sbjct: 482 DDCC 485

```
>gi|3011710|gb|AAC11158.1|I75569 Sequence 3 from patent US 5688764
Length = 39
```

Score = 18.5 bits (36), Expect = 365

Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXXC 20

DCCS C

Sbjct: 13 DCCSGSC 19

```
>gi|1613542|gb|AAB16522.1| Sequence 19 from patent US 5559095
gi|1830476|gb|AAB44930.1| Sequence 19 from patent US 5587454
gi|4000591|gb|AAC94023.1|AR024765 Sequence 19 from patent US 5795864
gi|5942586|gb|AAE02118.1| Sequence 19 from patent US 5859186
gi|5972579|gb|AAE12470.1| Sequence 19 from patent US 5824645
gi|7223980|gb|AAE24147.1| Sequence 19 from patent US 5891849
gi|10064318|gb|AAE38725.1| Sequence 19 from patent US 5994305
gi|12815643|gb|AAE45452.1| Sequence 19 from patent US 6087091
gi|14477881|gb|AAE61444.1| Sequence 19 from patent US 6136786
Length = 26
```

Score = 18.5 bits (36), Expect = 365  
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXSC 20  
DCCS C  
Sbjct: 14 DCCSGSC 20

>gi|1831302|gb|AAB45756.1| Sequence 3 from patent US 5591821  
Length = 26

Score = 18.5 bits (36), Expect = 365  
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXSC 20  
DCCS C  
Sbjct: 14 DCCSGSC 20

>gi|2725130|gb|AAB92812.1|I67150 Sequence 21 from patent US 5670319  
gi|3208874|gb|AAC20455.1|I80584 Sequence 21 from patent US 5708142  
gi|3991852|gb|AAC85279.1|AR002803 Sequence 21 from patent US 5741667  
gi|5951378|gb|AAE05604.1| Sequence 21 from patent US 5869612  
Length = 28

Score = 18.5 bits (36), Expect = 365  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 11 HLDDC 15  
HLD+C  
Sbjct: 24 HLDEC 28

>gi|4774193|emb|CAB42495.1| unnamed protein product [unidentified]  
Length = 2321

Score = 18.5 bits (36), Expect = 365  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 11 HLDDCC 16  
HLDD C  
Sbjct: 350 HLDDAC 355

>gi|413431|emb|CAA00767.1| ORF2 [synthetic construct]  
Length = 167

Score = 18.5 bits (36), Expect = 365  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 13 DDCC 16  
DDCC  
Sbjct: 36 DDCC 39

>gi|10049538|gb|AAE26445.1| Sequence 13 from patent US 5948900  
Length = 306

Score = 18.5 bits (36), Expect = 365  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 12 LDDCCS 17  
LDDC S  
Sbjct: 297 LDDCSS 302

>gi|12807911|gb|AAE43131.1| Sequence 4 from patent US 6074840  
Length = 1253

Score = 18.5 bits (36), Expect = 365  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 13 DDCC 16  
DDCC  
Sbjct: 1093 DDCC 1096

>gi|3011709|gb|AAC11157.1|I75568| Sequence 2 from patent US 5688764  
Length = 39

Score = 18.5 bits (36), Expect = 365  
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXXC 20  
DCCS C  
Sbjct: 13 DCCSGNC 19

>gi|21065678|emb|CAD32037.1| unnamed protein product [Homo sapiens]  
Length = 777

Score = 18.5 bits (36), Expect = 365  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 13 DDCCS 17  
D+CCS  
Sbjct: 35 DECCS 39

>gi|20241673|gb|AAE92344.1| Sequence 338 from patent US 6348328  
Length = 243

Score = 18.5 bits (36), Expect = 365  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 13 DDCC 16  
DDCC  
Sbjct: 240 DDCC 243

>gi|3994135|gb|AAC87563.1|AR007929| Sequence 16 from patent US 5750652

gi|12813714|gb|AAE45014.1| Sequence 19 from patent US 6083904  
Length = 2471

Score = 18.5 bits (36), Expect = 365  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 11 HLDDCC 16

HLDD C

Sbjct: 374 HLDDAC 379

Score = 18.5 bits (36), Expect = 365  
Identities = 6/13 (46%), Positives = 8/13 (61%)

Query: 8 CXQHLDDCCSXXC 20

C + LD+C S C

Sbjct: 1146 CEEQLDECASNPC 1158

>gi|18674249|emb|CAD23272.1| unnamed protein product [Homo sapiens]  
gi|21522704|emb|CAD35406.1| unnamed protein product [Homo sapiens]  
Length = 2470

Score = 18.5 bits (36), Expect = 365  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 11 HLDDCC 16

HLDD C

Sbjct: 373 HLDDAC 378

Score = 18.5 bits (36), Expect = 365  
Identities = 6/13 (46%), Positives = 8/13 (61%)

Query: 8 CXQHLDDCCSXXC 20

C + LD+C S C

Sbjct: 1145 CEEQLDECASNPC 1157

>gi|3994138|gb|AAC87566.1|AR007932 Sequence 19 from patent US 5750652  
Length = 2703

Score = 18.5 bits (36), Expect = 365  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 11 HLDDCC 16

HLDD C

Sbjct: 408 HLDDAC 413

Score = 14.6 bits (27), Expect = 5150  
Identities = 3/4 (75%), Positives = 4/4 (100%)

Query: 12 LDDC 15

LD+C

Sbjct: 1416 LDEC 1419

Score = 12.9 bits (23), Expect = 16694  
 Identities = 4/9 (44%), Positives = 6/9 (66%)

Query: 13 DDCCSXXCN 21  
 ++C S CN  
 Sbjct: 679 NECHSNPCN 687

>gi|3011708|gb|AAC11156.1|175567 Sequence 1 from patent US 5688764  
 Length = 39

Score = 18.5 bits (36), Expect = 365  
 Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXXC 20  
 DCCS C  
 Sbjct: 13 DCCSGNC 19

>gi|14097464|gb|AAE52306.1| Sequence 5 from patent US 6133232  
 Length = 979

Score = 18.5 bits (36), Expect = 365  
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 11 HLDDC 15  
 HLD+C  
 Sbjct: 798 HLDNC 802

Get selected sequences  
 Select all  
 Deselect all

Database: Protein sequences derived from the Patent division of  
 GenBank

Posted date: Nov 25, 2002 1:06 AM  
 Number of letters in database: 16,453,681  
 Number of sequences in database: 104,350

Lambda K H  
 0.357 0.284 2.14

Gapped  
 Lambda K H  
 0.294 0.110 0.610

Matrix: PAM30  
 Gap Penalties: Existence: 9, Extension: 1  
 Number of Hits to DB: 379,047  
 Number of Sequences: 104350  
 Number of extensions: 3808

Number of successful extensions: 641  
Number of sequences better than 20000.0: 623  
Number of HSP's better than 20000.0 without gapping: 623  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 641  
length of query: 27  
length of database: 16,453,681  
effective HSP length: 18  
effective length of query: 9  
effective length of database: 14,575,381  
effective search space: 131178429  
effective search space used: 131178429  
T: 11  
A: 40  
X1: 14 ( 7.2 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 23 (13.7 bits)  
S2: 23 (12.9 bits)

Search for :

CHIXNQHCWQHLDCCSHHCNHWNHCV

Chose to make the most divergent peptide (still within scope of generic) to test what would match.

### **BLASTP 2.2.4 [Aug-26-2002]**

#### **Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038288569-017646-1278

#### **Query=**

(27 letters)

**Database:** All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,242,768 sequences; 395,571,179 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

#### **Distribution of 157 Blast Hits on the Query Sequence**

---

Score (bits)	E Value
52	6e-07
29	4.5
28	15
27	26
27	35
27	35
27	35

Sequences producing significant alignments:

gi|3891872|pdb|1KCP| 3d Structure Of K-Conotoxin Pviia, A ... 52 6e-07  
gi|7519866|pir||A58997 kappa-conotoxin PVIIA - cone shell (... 52 6e-07  
gi|3891964|pdb|1AV3| Potassium Channel Blocker Kappa Conot... 52 6e-07  
gi|22002036|sp|P56633|CXK7 CONPU Kappa-conotoxin PVIIA prec... 52 6e-07  
gi|6907097|dbj|BAA90624.1| Similar to Arabidopsis thaliana ... 29 4.5  
gi|21402496|ref|NP\_658481.1| minC, Bacterial proteins invol... 28 15  
gi|13376410|ref|NP\_079212.1| hypothetical protein FLJ23024 ... 27 26  
gi|1085397|pir||S46487 taurine transporter - human >gi|5598... 27 35  
gi|1352535|sp|P31641|S6A6 HUMAN Sodium- and chloride-depend... 27 35  
gi|13560627|gb|AAK30132.1|AF346763\_1 intestinal taurine tra...

gi 23482928 gb EAA18766.1	hypothetical protein [Plasmodium...]	27	35
gi 4507045 ref NP_003034.1	solute carrier family 6 (neurot...)	27	35
gi 1708864 sp P98157 LRP1 CHICK	Low-density lipoprotein rec...	27	35
gi 13623303 gb AAH06252.1 AAH06252	Unknown (protein for MGC...)	27	35
gi 21105785 gb AAM34790.1 AF512560_2	HAC4 [Arabidopsis thal...]	26	47
gi 6010654 gb AAF01207.1 AF180526_1	E-septin short form [Ra...]	26	47
gi 18405622 ref NP_564706.1	CREB-binding protein, putative...	26	47
gi 14794966 gb AAK73519.1	HAC4 [Arabidopsis thaliana]	26	47
gi 13929200 ref NP_114025.1	E-septin [Rattus norvegicus] >...	26	47
gi 20093168 ref NP_619243.1	hypothetical protein (multi-do...)	26	47
gi 6090881 gb AAF03376.1 AF170253_1	septin-like protein [Ra...]	26	47
gi 6683817 gb AAF23374.1	MLL septin-like fusion protein MS...	26	47
gi 17560900 ref NP_506264.1	Predicted CDS, major sperm pro...	26	47
gi 8778322 gb AAF79331.1 AC002304_24	F14J16.27 [Arabidopsis...]	26	47
gi 5729933 ref NP_006631.1	MLL septin-like fusion; MLL sep...	26	47
gi 24656402 ref NP_611502.2	CG10438-PA [Drosophila melanog...	26	47
gi 22066365 ref XP_113892.2	similar to MLL septin-like fus...	26	47
gi 14530107 emb CAC42222.1	OVARIAN/Breast septin delta [Ho...]	26	47
gi 6056385 gb AAF02849.1 AC009894_20	Unknown protein [Arabi...]	26	47
gi 10433911 dbj BAB14057.1	unnamed protein product [Homo s...]	26	47
gi 8393784 ref NP_059076.1	septin 9; MLL septin-like fusio...	26	47
gi 14530105 emb CAC42221.1	OVARIAN/Breast septin gamma [Ho...]	26	47
gi 7512587 pir T12519	hypothetical protein DKFZp434F243.1 ...	26	47
gi 4589626 dbj BAA76835.1	KIAA0991 protein [Homo sapiens] ...	26	47
gi 18582088 ref XP_090617.1	similar to Adenylate cyclase, ...	26	47
gi 6090911 gb AAF03391.1 AF173899_1	septin-like protein SLP...	26	47
gi 20892533 ref XP_156144.1	hypothetical protein XP_156144...	26	47
gi 23058070 gb ZP_00083175.1	hypothetical protein [Pseudom...]	26	63
gi 24459580 gb AAN34381.1	envelope glycoprotein [Human imm...]	26	63
gi 20844494 ref XP_137952.1	similar to putative retrovirus...	26	63
gi 9629632 ref NP_044917.1	tegument protein/FGARAT [murid ...]	26	63
gi 23272552 gb AAH35574.1	chromosome 6 open reading frame ...	26	63
gi 13449287 ref NP_085155.1	NG3 protein [Homo sapiens] >gi...	26	63
gi 16924037 gb AAL31649.1 AC079179_4	Putative o-methyltran...	25	85
gi 23472065 gb ZP_00127393.1	hypothetical protein [Pseudom...]	25	85
gi 20908811 ref XP_138742.1	similar to endogenous retrovir...	25	85
gi 15598375 ref NP_251869.1	conserved hypothetical protein...	25	85
gi 23058698 gb ZP_00083733.1	hypothetical protein [Pseudom...]	25	85
gi 20468866 ref XP_117141.1	hypothetical protein XP_117141...	25	85
gi 15983410 gb AAL11573.1 AF424579_1	AT4g16570/dl4310w [Ara...]	25	114
gi 22094360 gb AAM91887.1	putative cytokinin oxidase [Oryz...]	25	114
gi 202106 gb AAA40468.1	transition protein 2' (alt.)	25	114
gi 110055 pir IS14529	transition protein 2 - mouse >gi 5487...	25	114
gi 18414696 ref NP_567508.1	expressed protein; protein id:...	25	114
gi 21302270 gb EAA14415.1	agCP8608 [Anopheles gambiae str....]	25	114
gi 24817521 emb CAD54147.2	Hypothetical protein ZK757.4 [C...	25	114
gi 202105 gb AAA40467.1	transition protein 2 (alt.) >gi 12...	25	114
gi 17557071 ref NP_499189.1	DHHC zinc binding domain conta...	25	114
gi 12083591 ref NP_038722.2	transition protein 2 [Mus musc...]	25	114
gi 24646280 ref NP_650191.1	CG5196-PA [Drosophila melanoga...	25	114
gi 15836695 ref NP_297383.1	tRNA delta(2)-isopentenylpyrop...	25	114
gi 20151945 gb AAM11332.1	GH06759p [Drosophila melanogaster]	25	114
gi 16519539 ref NP_443737.1	low density lipoprotein-relate...	25	114
gi 23055343 gb ZP_00081453.1	hypothetical protein [Geobact...	25	114
gi 13937291 gb AAK50122.1 AC087797_7	putative phospholipase...	25	114
gi 930024 emb CAA30824.1	tenascin [Gallus gallus]	24	153
gi 135584 sp P10039 TENA CHICK	Tenascin precursor (TN) (Hex...	24	153
gi 15230656 ref NP_187904.1	putative CREB-binding protein;...	24	153
gi 212748 gb AAA49085.1	190 kd tenascin precursor	24	153
gi 18546360 ref XP_099257.1	hypothetical protein XP_099257...	24	153
gi 212747 gb AAA49084.1	200 kd tenascin precursor	24	153

gi 21105780 gb AAM34788.1 AF512558_2	HAC5 [Arabidopsis thal...	24	153
gi 15341664 gb AAH06778.1	Unknown (protein for IMAGE:35890...	24	205
gi 2507193 sp P27704 MK06	RAT Mitogen-activated protein kin...	24	205
gi 13928856 ref NP_113810.1	mitogen-activated protein kina...	24	205
gi 24583179 ref NP_609327.2	CG31712-PA [Drosophila melanog...	24	205
gi 22049606 ref XP_070277.2	similar to Otoconin 90 precurs...	24	205
gi 23592724 ref XP_128141.2	otoconin 90 [Mus musculus]	24	205
gi 4506139 ref NP_002759.1	procollagen (type III) N-endope...	24	205
gi 22996345 gb ZP_00040604.1	hypothetical protein [Xylella...	24	205
gi 22993598 gb ZP_00038168.1	hypothetical protein [Xylella...	24	205
gi 13509205 emb CAC35209.1	GRAAL2 protein [Drosophila mela...	24	205
gi 6682303 emb CAB64653.1	GRAAL protein [Drosophila melano...	24	205
gi 7488985 pir T17462	disease resistance E - tomato >gi 42...	24	205
gi 15292455 gb AAK93496.1	SD02860p [Drosophila melanogaster]	24	205
gi 18593306 ref XP_104434.1	hypothetical protein XP_104434...	24	205
gi 21430770 gb AAM51063.1	SD13780p [Drosophila melanogaster]	24	205
gi 4092677 gb AAC99455.1	otoconin-90 [Mus musculus]	24	205
gi 17464262 ref XP_069418.1	hypothetical protein XP_069418...	24	205
gi 16416462 dbj BAB70658.1	spondin [Ciona savignyi]	24	205
gi 4176764 gb AAD08924.1	otoconin-95 precursor [Mus musculus]	24	205
gi 16762646 ref NP_458263.1	alpha-amylase [Salmonella ente...	24	205
gi 23239621 gb AAH35492.1	similar to mitogen-activated pro...	24	205
gi 18858913 ref NP_571936.1	jagged1 [Danio rerio] >gi 2045...	24	205
gi 16766949 ref NP_462564.1	alpha-amylase [Salmonella typh...	24	205
gi 4506091 ref NP_002739.1	mitogen-activated protein kinas...	24	205
gi 6225792 sp Q02509 OC90	HUMAN Otoconin 90 precursor (Oc90...	24	205
gi 559705 dbj BAA07557.1	The ha1551 gene is novel. [Homo s...	24	205
gi 24661359 ref NP_648288.1	CG4821-PA [Drosophila melanoga...	24	205
gi 59977 emb CAA78662.1	tripartite fusion transcript PLA2L...	24	205

### Alignments

Get selected sequences

Select all

Deselect all

>gi|3891872|pdb|1KCP| 3d Structure Of K-Conotoxin Pviia, A Novel Potassium

Channel-Blocking Toxin From Cone Snails, Nmr, 22

Structures

Length = 28

Score = 52.4 bits (116), Expect = 6e-07

Identities = 19/27 (70%), Positives = 21/27 (77%)

Query: 1 CHIXNQHCWQHLDCCSHHCNHNHCV 27

C I NQ C+QHLDCCS CN +N CV

Sbjct: 1 CRIXNQKCFQHLDCCSRKCNRFNKC 27

>gi|7519866|pir||A58997 kappa-conotoxin PVIIA - cone shell (Conus purpurascens)

Length = 27

Score = 52.4 bits (116), Expect = 6e-07

Identities = 18/27 (66%), Positives = 20/27 (74%)

Query: 1 CHIXNQHCWQHLDCCSHHCNHNHCV 27

C I NQ C+QHLDCCS CN +N CV

Subjct: 1 CRI~~P~~NQKCFQH~~L~~DDCCSRKCNRFNKCV 27

>gi|3891964|pdb|1AV3| Potassium Channel Blocker Kappa Conotoxin Pviia From C. Purpurascens, Nmr, 20 Structures  
Length = 27

Score = 52.4 bits (116), Expect = 6e-07  
Identities = 19/27 (70%), Positives = 21/27 (77%)

Query: 1 CHIXNQHCWQH~~L~~DDCCSHHCNHNHCV 27  
C I NQ C+QH~~L~~DDCCS CN +N CV  
Subjct: 1 CRI~~P~~NQKCFQH~~L~~DDCCSRKCNRFNKCV 27

>gi|22002036|sp|P56633|CXK7 CONPU Kappa-conotoxin PVIIA precursor (Fin-popping peptide)  
Length = 72

Score = 52.4 bits (116), Expect = 6e-07  
Identities = 18/27 (66%), Positives = 20/27 (74%)

Query: 1 CHIXNQHCWQH~~L~~DDCCSHHCNHNHCV 27  
C I NQ C+QH~~L~~DDCCS . CN +N CV  
Subjct: 46 CRI~~P~~NQKCFQH~~L~~DDCCSRKCNRFNKCV 72

>gi|6907097|dbj|BAA90624.1| Similar to Arabidopsis thaliana DNA chromosome 4, ESSA I contig  
fragment No. 6; calcium channel protein alpha-1 chain isoform A - rat. (Z97341) [Oryza sativa (japonica cultivar-group)]  
Length = 589

Score = 29.5 bits (62), Expect = 4.5  
Identities = 8/15 (53%), Positives = 9/15 (60%), Gaps = 4/15 (26%)

Query: 17 SHH----CNHNHCV 27  
SHH C+HW CV  
Subjct: 292 SHHMKDWCDHWKQCV 306

>gi|21402496|ref|NP\_658481.1| minC, Bacterial proteins involved in chromosomal partitioning  
[Bacillus anthracis A2012]  
Length = 228

Score = 27.8 bits (58), Expect = 15  
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 11 HLDDCCS 17  
HLDDCCS  
Subjct: 21 HLDDCCS 27

>gi|13376410|ref|NP\_079212.1| hypothetical protein FLJ23024 [Homo sapiens]  
gi|10439583|dbj|BAB15524.1| unnamed protein product [Homo sapiens]

Length = 279

Score = 26.9 bits (56), Expect = 26  
 Identities = 11/30 (36%), Positives = 11/30 (36%), Gaps = 17/30 (56%)

Query: 5 NQHCWQHLDCCSHHCN-----WNHC 26  
 NQHC HCN WNHC  
 Sbjct: 157 NQHC-----EHCNSCTSKDGRKWNHC 177

>gi|1085397|pir||S46487 taurine transporter - human  
gi|559853|gb|AAA50842.1| placental taurine transporter  
 Length = 620

Score = 26.5 bits (55), Expect = 35  
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 19 HCNH-WN--HC 26  
 HCNH WN HC  
 Sbjct: 161 HCNHSWNTPHC 171

>gi|1352535|sp|P31641|S6A6 HUMAN Sodium- and chloride-dependent taurine transporter  
gi|7441660|pir||G01426 taurine transporter - human  
gi|799339|gb|AAC50443.1| taurine transporter  
 Length = 620

Score = 26.5 bits (55), Expect = 35  
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 19 HCNH-WN--HC 26  
 HCNH WN HC  
 Sbjct: 161 HCNHSWNTPHC 171

>gi|13560627|gb|AAK30132.1|AF346763\_1 intestinal taurine transporter [Homo sapiens]  
 Length = 244

Score = 26.5 bits (55), Expect = 35  
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 19 HCNH-WN--HC 26  
 HCNH WN HC  
 Sbjct: 81 HCNHSWNTPHC 91

>gi|23482928|gb|EAA18766.1| hypothetical protein [Plasmodium yoelii yoelii]  
 Length = 456

Score = 26.5 bits (55), Expect = 35  
 Identities = 11/24 (45%), Positives = 11/24 (45%), Gaps = 12/24 (50%)

Query: 6 QHCWQHLDCCSHHC-N--HWNHC 26  
 QH WQH C N HW HC  
 Sbjct: 188 QH-WQH-----CQNFQHWQHC 202

>gi|4507045|ref|NP\_003034.1| solute carrier family 6 (neurotransmitter transporter, taurine),  
 member 6; Solute carrier family 6 (neurotransmitter transporter, taurine), [Homo sapiens]  
gi|346388|pir|S29839| taurine transport protein - human  
gi|36727|emb|CAA79481.1| taurine transporter [Homo sapiens]  
gi|266092|gb|AAB25509.1| taurine transporter, HTAU [human, thyroid cells, Peptide, 619  
 aa]  
 Length = 619

Score = 26.5 bits (55), Expect = 35  
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 19 HCNH-WN--HC 26  
 HCNH WN HC  
 Sbjct: 161 HCNHSWNTPHC 171

>gi|1708864|sp|P98157|LRP1 CHICK Low-density lipoprotein receptor-related protein 1  
 precursor (LRP)  
 (Alpha-2-macroglobulin receptor) (A2MR)  
gi|1079416|pir||A53102| alpha-2-macroglobulin receptor precursor - chicken  
gi|438007|emb|CAA52870.1| alpha-2-macroglobulin receptor [Gallus gallus]  
 Length = 4543

Score = 26.5 bits (55), Expect = 35  
 Identities = 8/18 (44%), Positives = 10/18 (55%), Gaps = 4/18 (22%)

Query: 7 HCWQHLDDC----CSHHC 20  
 HC + L +C C HHC  
 Sbjct: 109 HCREQLANCTALGCQHHC 126

>gi|13623303|gb|AAH06252.1|AAH06252| Unknown (protein for MGC:10619) [Homo sapiens]  
 Length = 200

Score = 26.5 bits (55), Expect = 35  
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 19 HCNH-WN--HC 26  
 HCNH WN HC  
 Sbjct: 161 HCNHSWNTPHC 171

>gi|21105785|gb|AAM34790.1|AF512560\_2| HAC4 [Arabidopsis thaliana]  
 Length = 385

Score = 26.1 bits (54), Expect = 47  
 Identities = 11/25 (44%), Positives = 11/25 (44%), Gaps = 10/25 (40%)

Query: 11 HLDDCCSHHC-----NHW--NHC 26  
 HL CC HC N W NHC  
 Sbjct: 90 HLQHCCK-HCTTLMVSGNRWVCNHC 113

>gi|6010654|gb|AAF01207.1|AF180526\_1| E-septin short form [Rattus norvegicus]

Length = 334

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 118 HINNENCWQ 126

>gi|18405622|ref|NP\_564706.1| CREB-binding protein, putative; protein id: At1g55970.1,  
 supported by  
 cDNA: gi\_14794965 [Arabidopsis thaliana]  
 Length = 1456

Score = 26.1 bits (54), Expect = 47  
 Identities = 11/25 (44%), Positives = 11/25 (44%), Gaps = 10/25 (40%)

Query: 11 HLDDCCSHHC-----NHW--NHC 26  
 HL CC HC N W NHC  
 Sbjct: 1161 HLQHCCK-HCTTLMVSGNRWVCNHC 1184

>gi|14794966|gb|AAK73519.1| HAC4 [Arabidopsis thaliana]  
 Length = 413

Score = 26.1 bits (54), Expect = 47  
 Identities = 11/25 (44%), Positives = 11/25 (44%), Gaps = 10/25 (40%)

Query: 11 HLDDCCSHHC-----NHW--NHC 26  
 HL CC HC N W NHC  
 Sbjct: 118 HLQHCCK-HCTTLMVSGNRWVCNHC 141

>gi|13929200|ref|NP\_114025.1| E-septin [Rattus norvegicus]  
gi|6010652|gb|AAF01206.1|AF180525\_1 E-septin long form [Rattus norvegicus]  
 Length = 405

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 189 HINNENCWQ 197

>gi|20093168|ref|NP\_619243.1| hypothetical protein (multi-domain) [Methanosa  
 cina acetivorans  
 str. C2A]  
gi|19918512|gb|AAM07723.1| hypothetical protein (multi-domain) [Methanosa  
 cina acetivorans  
 str. C2A]  
 Length = 489

Score = 26.1 bits (54), Expect = 47  
 Identities = 8/14 (57%), Positives = 9/14 (64%)

Query: 14 DCCSHHCNHWNHCV 27  
 DCC H C+H H V  
 Sbjct: 463 DCCCHECDHHKHYV 476

>gi|6090881|gb|AAF03376.1|AF170253 1 septin-like protein [Rattus norvegicus]  
 Length = 564

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 349 HINNENCWQ 357

>gi|6683817|gb|AAF23374.1| MLL septin-like fusion protein MSF-A [Homo sapiens]  
 Length = 586

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 369 HINNENCWQ 377

>gi|17560900|ref|NP\_506264.1| Predicted CDS, major sperm protein family member family  
 member

[Caenorhabditis elegans]

gi|7503252|pir|T22096 hypothetical protein F42E8.2 - Caenorhabditis elegans  
gi|3877039|emb|CAB01429.1| Hypothetical protein F42E8.2 [Caenorhabditis elegans]  
 Length = 122

Score = 26.1 bits (54), Expect = 47  
 Identities = 8/12 (66%), Positives = 8/12 (66%), Gaps = 2/12 (16%)

Query: 13 DDCCSHHCNHW 24  
 D CCSH C WN  
 Sbjct: 96 DACCSHSC--WN 105

>gi|8778322|gb|AAF79331.1|AC002304 24 F14J16.27 [Arabidopsis thaliana]  
 Length = 1550

Score = 26.1 bits (54), Expect = 47  
 Identities = 11/25 (44%), Positives = 11/25 (44%), Gaps = 10/25 (40%)

Query: 11 HLDDCCSHC-----NHW--NHC 26  
 HL CC HC N W NHC  
 Sbjct: 1229 HLQHCCK-HCTTLMVSGNRWVCNHC 1252

>gi|5729933|ref|NP\_006631.1| MLL septin-like fusion; MLL septin-like fusion (NOTE: non-  
 standard  
 symbol and name); septin D1 [Homo sapiens]

gi|5106557|gb|AAD39749.1|AF123052\_1 MLL septin-like fusion protein [Homo sapiens]  
gi|11055011|gb|AAG27919.1|AF142408\_1 cell division control protein septin D1 [Homo sapiens]  
gi|14530109|emb|CAC42223.1| OVARIAN/Breast septin alpha [Homo sapiens]  
gi|18203688|gb|AAH21192.1|AAH21192 MLL septin-like fusion [Homo sapiens]  
Length = 568

Score = 26.1 bits (54), Expect = 47  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
HI N++CWQ  
Sbjct: 351 HINNENCWQ 359

>gi|24656402|ref|NP\_611502.2| CG10438-PA [Drosophila melanogaster]  
gi|24656406|ref|NP\_725988.1| CG30144-PA [Drosophila melanogaster]  
gi|7302348|gb|AAF57437.1| CG10438-PA [Drosophila melanogaster]  
gi|21626895|gb|AAM68396.1| CG30144-PA [Drosophila melanogaster]  
Length = 108

Score = 26.1 bits (54), Expect = 47  
Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 1/10 (10%)

Query: 15 CCSHHCNH-W 23  
CC+H CNH W  
Sbjct: 97 CCNHECNHTW 106

>gi|22066365|ref|XP\_113892.2| similar to MLL septin-like fusion; MLL septin-like fusion  
(NOTE:  
non-standard symbol and name); septin D1 [Homo sapiens]  
Length = 569

Score = 26.1 bits (54), Expect = 47  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
HI N++CWQ  
Sbjct: 352 HINNENCWQ 360

>gi|14530107|emb|CAC42222.1| OVARIAN/Breast septin delta [Homo sapiens]  
Length = 335

Score = 26.1 bits (54), Expect = 47  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
HI N++CWQ  
Sbjct: 118 HINNENCWQ 126

>gi|6056385|gb|AAF02849.1|AC009894\_20 Unknown protein [Arabidopsis thaliana]  
Length = 1209

Score = 26.1 bits (54), Expect = 47

Identities = 11/25 (44%), Positives = 11/25 (44%), Gaps = 10/25 (40%)

Query: 11 HLDDCCSHHC-----NHW--NHC 26  
 HL CC HC N W NHC  
 Sbjct: 1152 HLQHCCK-HCTTLMVSGNRWVCNHC 1175

>gi|10433911|dbj|BAB14057.1| unnamed protein product [Homo sapiens]  
 Length = 196

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 118 HINNENCWQ 126

>gi|8393784|ref|NP\_059076.1| septin 9; MLL septin-like fusion; SL3-3 integration site 1  
 [Mus  
 musculus]  
gi|20347564|ref|XP\_109283.1| MLL septin-like fusion [Mus musculus]  
gi|6165419|emb|CAB59833.1| septin-like protein Sint1 [Mus musculus]  
gi|17980682|gb|AAL50685.1| septin 9 [Mus musculus]  
 Length = 334

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 118 HINNENCWQ 126

>gi|14530105|emb|CAC42221.1| OVARIAN/Breast septin gamma [Homo sapiens]  
 Length = 579

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 362 HINNENCWQ 370

>gi|7512587|pir|T12519 hypothetical protein DKFZp434F243.1 - human (fragment)  
gi|5262571|emb|CAB45728.1| hypothetical protein [Homo sapiens]  
 Length = 234

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 17 HINNENCWQ 25

>gi|4589626|dbj|BAA76835.1| KIAA0991 protein [Homo sapiens]  
gi|6683815|gb|AAF23373.1| MLL septin-like fusion protein MSF-B [Homo sapiens]  
gi|14530111|emb|CAC42224.1| OVARIAN/Breast septin beta [Homo sapiens]  
Length = 422

Score = 26.1 bits (54), Expect = 47  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
HI N++CWQ  
Sbjct: 205 HINNENCWQ 213

>gi|18582088|ref|XP\_090617.1| similar to Adenylate cyclase, type VII (ATP pyrophosphate-lyase)  
(Adenyllyl cyclase) [Homo sapiens]  
Length = 180

Score = 26.1 bits (54), Expect = 47  
Identities = 7/12 (58%), Positives = 7/12 (58%), Gaps = 2/12 (16%)

Query: 7 HCWQHLDCCSH 18  
CWQ DCCS  
Sbjct: 25 QCWQR--DCCSQ 34

Score = 18.0 bits (35), Expect = 12551  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 5 NQHC 8  
NQHC  
Sbjct: 148 NQHC 151

>gi|6090911|gb|AAF03391.1|AF173899 1 septin-like protein SLP-b [Rattus norvegicus]  
Length = 479

Score = 26.1 bits (54), Expect = 47  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
HI N++CWQ  
Sbjct: 264 HINNENCWQ 272

>gi|20892533|ref|XP\_156144.1| hypothetical protein XP\_156144 [Mus musculus]  
Length = 213

Score = 26.1 bits (54), Expect = 47  
Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 5 NQHCWQHL 12  
NQ CW+HL  
Sbjct: 40 NQRCWEHL 47

>gi|23058070|gb|ZP\_00083175.1| hypothetical protein [Pseudomonas fluorescens]  
 Length = 176

Score = 25.7 bits (53), Expect = 63  
 Identities = 8/15 (53%), Positives = 8/15 (53%), Gaps = 5/15 (33%)

Query: 6 QHCWQHLDCCSHHC 20  
 Q CW CCSH C  
 Sbjct: 164 QRCW-----CCSHCC 173

>gi|24459580|gb|AAN34381.1| envelope glycoprotein [Human immunodeficiency virus 1]  
 Length = 211

Score = 25.7 bits (53), Expect = 63  
 Identities = 7/11 (63%), Positives = 7/11 (63%), Gaps = 4/11 (36%)

Query: 19 HCN----HWNH 25  
 HCN HWNH  
 Sbjct: 63 HCNISKGHWNH 73

>gi|20844494|ref|XP\_137952.1| similar to putative retrovirus-related gag protein [Mus  
 musculus]

Length = 212

Score = 25.7 bits (53), Expect = 63  
 Identities = 7/11 (63%), Positives = 8/11 (72%), Gaps = 1/11 (9%)

Query: 2 HIXNQHCWQHL 12  
 HI NO CW+ L  
 Sbjct: 31 HI-NQQCWERL 40

>gi|9629632|ref|NP\_044917.1| tegument protein/FGARAT [murid herpesvirus 4]

gi|2318002|gb|AAB66460.1| tegument protein/FGARAT [murid herpesvirus 4]

gi|6625640|gb|AAF19341.1|AF105037 73 75a [murid herpesvirus 4]

Length = 1291

Score = 25.7 bits (53), Expect = 63  
 Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 9 WQHLDD 14  
 WQHLDD  
 Sbjct: 1261 WQHLDD 1266

>gi|23272552|gb|AAH35574.1| chromosome 6 open reading frame 8 [Homo sapiens]  
 Length = 293

Score = 25.7 bits (53), Expect = 63  
 Identities = 10/22 (45%), Positives = 12/22 (54%), Gaps = 10/22 (45%)

Query: 7 HCWQHLD--DC-----CSHHC 20  
 HC H+D +C CSHHC

Sbjct: 140 HC--HVDVDECRTSITLCSHHC 159

>gi|13449287|ref|NP\_085155.1| NG3 protein [Homo sapiens]  
gi|1841553|gb|AAB47494.1|AAB47494 NG3 [Homo sapiens]  
 Length = 293

Score = 25.7 bits (53), Expect = 63  
 Identities = 10/22 (45%), Positives = 12/22 (54%), Gaps = 10/22 (45%)

Query: 7 HCWQHLD--DC-----CSHHC 20  
 HC H+D +C CSHHC

Sbjct: 140 HC--HVDVDECRTSITLCSHHC 159

>gi|16924037|gb|AAL31649.1|AC079179 4 Putative o-methyltransferase ZRP4 [Oryza sativa]  
gi|17047043|gb|AAL34948.1|AC079037 21 Putative o-methyltransferase ZRP4 [Oryza sativa]  
 Length = 366

Score = 25.2 bits (52), Expect = 85  
 Identities = 7/9 (77%), Positives = 7/9 (77%), Gaps = 1/9 (11%)

Query: 7 HCWQHLDDC 15  
 HCWQ DDC

Sbjct: 271 HCWQD-DDC 278

>gi|23472065|gb|ZP\_00127393.1| hypothetical protein [Pseudomonas syringae pv. syringae B728a]  
 Length = 409

Score = 25.2 bits (52), Expect = 85  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 21 NHWNHCV 27  
 NHW HCV

Sbjct: 194 NHWYHCV 200

>gi|20908811|ref|XP\_138742.1| similar to endogenous retroviral family W, env(C7), member 1  
 (syncytin); envelope protein; syncytin [Homo sapiens]  
 [Mus musculus]  
 Length = 712

Score = 25.2 bits (52), Expect = 85  
 Identities = 12/26 (46%), Positives = 12/26 (46%), Gaps = 8/26 (30%)

Query: 1 CHIXNQHCWQHLDCCSHHCNHNHC 26  
 CH HC Q L D C HH HC  
 Sbjct: 34 CH---HHCLQPLLDSCHHH----HC 51

>gi|15598375|ref|NP\_251869.1| conserved hypothetical protein [Pseudomonas aeruginosa PA01]

gi|11347983|pir||E83247 conserved hypothetical protein PA3179 [imported] - *Pseudomonas aeruginosa* (strain PAO1)  
gi|9949297|gb|AAG06567.1|AE004742 3 conserved hypothetical protein [Pseudomonas aeruginosa PAO1]  
Length = 386

Score = 25.2 bits (52), Expect = 85  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 21 NHWNHCV 27  
NHW HCV  
Sbjct: 191 NHWYHCV 197

>gi|23058698|gb|ZP\_00083733.1| hypothetical protein [Pseudomonas fluorescens]  
Length = 448

Score = 25.2 bits (52), Expect = 85  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 21 NHWNHCV 27  
NHW HCV  
Sbjct: 237 NHWYHCV 243

>gi|20468866|ref|XP\_117141.1| hypothetical protein XP\_117141 [Homo sapiens]  
Length = 169

Score = 25.2 bits (52), Expect = 85  
Identities = 8/13 (61%), Positives = 10/13 (76%), Gaps = 1/13 (7%)

Query: 15 CC-SHHCNHNHC 26  
CC SHH +H +HC  
Sbjct: 128 CCLSHHRHRSHC 140

>gi|15983410|gb|AAL11573.1|AF424579 1 AT4g16570/dl4310w [Arabidopsis thaliana]  
gi|23308405|gb|AAN18172.1| At4g16570/dl4310w [Arabidopsis thaliana]  
Length = 457

Score = 24.8 bits (51), Expect = 114  
Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 20 CNHWNHCV 27  
C+HW CV  
Sbjct: 82 CDHWKQCV 89

Get selected sequences  
Select all  
Deselect all

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF  
Posted date: Nov 25, 2002 1:38 AM  
Number of letters in database: 395,571,179

Number of sequences in database: 1,242,768

Lambda	K	H
0.359	0.268	2.40

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Hits to DB: 17,703,379

Number of Sequences: 1242768

Number of extensions: 331126

Number of successful extensions: 8258

Number of sequences better than 20000.0: 8042

Number of HSP's better than 20000.0 without gapping: 8050

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 8242

length of query: 27

length of database: 395,571,179

effective HSP length: 18

effective length of query: 9

effective length of database: 373,201,355

effective search space: 3358812195

effective search space used: 3358812195

T: 11

A: 40

X1: 14 ( 7.3 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 34 (19.5 bits)

S2: 34 (17.6 bits)



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No.	Doccode	Number of pages
1	C.AD	1✓

Total number of pages: 1

Remarks:

Order of re-scan issued on .....